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OM protein - protein search, using sw model

Run on: August 18, 2002, 08:18:46 ; Search time 61.25 Seconds  
(without alignments)  
865.016 Million cell updates/sec

Title: US-09-777-921A-2

Perfect score: 2481

Sequence: 1 MLRMLRDPALPTAACQDAEQ.....VGISVYVENKQTLGVYQK 477

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A.Geneseq\_032802:\*
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  - 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*
  - 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
  - 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2471	99.6	477	22	AAW79077
2	1552.5	62.6	471	22	AAU27697
3	1552.5	62.6	509	22	AAU27869
4	1501	60.5	469	22	AAV66718
5	1501	60.5	469	22	AAAB8754
6	1501	60.5	469	22	AAAB5241
7	1499	60.4	469	21	AAV76084
8	1499	60.4	469	22	AAAB56023
9	1479.5	59.6	508	22	ABG22637
10	1394	56.2	385	21	AAAB2329
11	1325	53.4	366	22	AAAB40072

12	1241	50.0	461	22	AA65800	Human membrane tra
13	1143	46.1	244	22	AAAB3524	Human polypeptide
14	1143	46.1	244	22	AAU19941	Novel human calcit
15	1037	41.8	292	21	AAAB50388	Human uncoupling p
16	910	36.7	312	22	AAV75964	Murine skin cell p
17	910	36.7	312	22	AAAB55903	Skin cell protein,
18	902	36.4	370	22	ABAB71306	Drosophila melanog
19	841	33.9	182	22	AAAB60061	Human protein SEQ
20	800.5	32.3	226	22	AAAB1858	Human polypeptide
21	761	30.7	208	22	AAAB3247	Human polypeptide,
22	632	25.5	169	21	AAAB50389	Human uncoupling p
23	521	21.0	352	21	AAAG30070	Arabidopsis thalia
24	508	20.5	241	21	AAAG12158	Arabidopsis thalia
25	508	20.5	330	21	AAAG28434	Arabidopsis thalia
26	508	20.5	332	21	AAAG28433	Arabidopsis thalia
27	505.5	20.4	166	21	AAAB2319	Human OREF2083
28	479	19.3	138	22	ABG22634	Novel human diagno
29	455.5	18.4	415	21	AAAG29005	Arabidopsis thalia
30	454.5	18.3	289	20	AAV11936	Wheat brittle-1 pa
31	454.5	18.3	381	21	AAAG29257	Arabidopsis thalia
32	454.5	18.3	384	21	AAAG29256	Arabidopsis thalia
33	446	18.0	392	21	AAAG11515	Arabidopsis thalia
34	446	18.0	392	21	AAAG49411	Arabidopsis thalia
35	446	18.0	411	21	AAAG11514	Arabidopsis thalia
36	446	18.0	411	21	AAAG49410	Arabidopsis thalia
37	445	17.9	291	21	AAAG30071	Arabidopsis thalia
38	432.5	17.4	316	21	AAAG11516	Arabidopsis thalia
39	432.5	17.4	316	21	AAAG49412	Arabidopsis thalia
40	417	16.8	198	21	AAAG12159	Arabidopsis thalia
41	412	16.6	266	21	AAAG28435	Arabidopsis thalia
42	410.5	16.5	377	22	ABAB60506	Drosophila melanog
43	382.5	15.4	273	21	AAAG29006	Arabidopsis thalia
44	380.5	15.3	267	21	AAAG29258	Arabidopsis thalia
45	369	14.9	323	22	AAAB41427	Human polypeptide

ALIGNMENTS

RESULT 1	
ID AAM79077	standard; Protein: 477 AA.
XX AAM79077:	
DT 06-NOV-2001	(first entry)
XX	
DE Human protein SEQ ID NO 1739.	
XX	
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;	
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;	
KW tissue growth factor; immunomodulatory; cancer; leukaemia;	
KW nervous system disorder; arthritis; inflammation.	
XX	
OS Homo sapiens.	
XX	
PN WO200157190-A2.	
PD	
XX 09-AUG-2001.	
PF	
XX 05-FEB-2001: 2001WO-US04098.	
XX	
PR 03-FEB-2000: 2000US-0496914.	
PR 27-APR-2000: 2000US-0560875.	
PR 20-JUN-2000: 2000US-0598075.	
PR 19-JUL-2000: 2000US-0620325.	
PR 01-SEP-2000: 2000US-0654936.	
PR 15-SEP-2000: 2000US-0663561.	
PR 20-OCT-2000: 2000US-0693325.	
PR 30-NOV-2000: 2000US-0728422.	
XX	
PA (HYSE-) HYSEO INC.	
XX	

PI Tang YF, Liu C, Dirmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
PI Zhao QA, Wang D, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Wehrman T, Goodrich R;  
XX WPI: 2001-476283/51.  
DR N-PSDB: AAK52210.  
XX  
XX Nucleic acids encoding polypeptides with cytokine-like activities,  
PI useful in diagnosis and gene therapy -  
PS Claim 20; Page 4074-4075; 6221pp; English.  
XX  
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation.  
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
CC (AAM80020) are omitted as the relevant pages from the sequence listing  
CC were missing at the time of publication.  
XX  
XX  
SQ Sequence 477 AA;

Query Match 99.6%; Score 2471; DB 22; Length 477;  
Best Local Similarity 99.6%; Pred. No. 1.8e-217;  
Matches 475; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 MRRLRDLFLPTAAQODAPRTRETLRQALDRNGGVYDICELOGELNLGPIGQDAE 60  
DB 1 MRLVRLDVLPLAACQDAEPQMLYELLIGALDRNGGVYDICELOGELNLGPIGQDAE 60  
OY 61 EKIFTTGVNKGDKLDFEEMFKYLYKDKHEKMKLAFKSLDKNDNGKLEASEIYOSLDTGL 120  
DB 61 EKIFTTGVNKGDKLDFEEMFKYLYKDKHEKMKLAFKSLDKNDNGKLEASEIYOSLDTGL 120  
OY 121 TISEQDAELILOSIDVGTVMVDMNEMRDYFLPNVTDIEEIRREKHSSTGIDIGSLTI 180  
DB 121 TISEQDAELILOSIDVGTVMVDMNEMRDYFLPNVTDIEEIRREKHSSTGIDIGSLTI 180  
OY 181 PDEFDEDEKSGOWMROLAAGIAGAVSRTAPLDRLKIMMOVHGSKSDKXNIFEGFRO 240  
DB 181 PDEFDEDEKSGOWMROLAAGIAGAVSRTAPLDRLKIMMOVHGSKSDKXNIFEGFRO 240  
OY 241 MVEEGGIRSLMNGNCTNVIKIPETAFAVKEAYEYKRLTEBQKIGTREFISGSMAGA 300  
DB 241 MVEEGGIRSLMNGNCTNVIKIPETAFAVKEAYEYKRLTEBQKIGTREFISGSMAGA 300  
OY 301 TQOTFTYPMWVKTRIAVAKTGOYSIDYCAKKILKHEGLGAFYKGYVNLGIYPAI 360  
DB 301 TQOTFTYPMWVKTRIAVAKTGOYSIDYCAKKILKHEGLGAFYKGYVNLGIYPAI 360  
OY 361 DIAYVELKSYMLDNFAKXSVNPGVWVLGCGALSTGCOLASYPALVTRTRNOQAAME 420  
DB 361 DIAYVELKSYMLDNFAKXSVNPGVWVLGCGALSTGCOLASYPALVTRTRNOQAAME 420  
OY 421 GSPQLMVMGLFRRIISKEGIPGLYRGITPNEFKVLPVAVGISYVYVBNMKOTLGVTOK 477  
DB 421 GSPQLMVMGLFRRIISKEGIPGLYRGITPNEFKVLPVAVGISYVYVBNMKOTLGVTOK 477

RESULT 2  
AAU27697  
ID AAU27697 standard; Protein; 471 AA.  
XX  
XX AAU27697;  
XX

DT 18-DEC-2001 (first entry)  
XX  
XX Human full-length polypeptide sequence #22.  
DE  
XX Mammal: human; rhesus monkey; baker's yeast; fission yeast; Norway rat;  
KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;  
KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;  
KW nervous system disorder; inflammatory disorder; cell differentiation;  
KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;  
KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;  
KW cytostatic; antineoplastic; antiarthritis; vulnery; antiinflammatory;  
KW antibacterial; immunosuppressive; vasotropic; antiparinsonian;  
KW neuroprotective; osteoprotic; antidiabetic; antiaustmatic; allergic;  
KW immunostimulant; analgesic; gene therapy.  
XX  
XX Homo sapiens.  
PN WO200164834-A2.  
XX  
XX  
PD 07-SEP-2001.  
XX  
XX 26-FEB-2001; 2001WO-US04926.  
XX  
XX 28-FEB-2000; 2000US-0515126.  
PR 18-MAY-2000; 2000US-0577409.  
PR 17-JUN-2000; 2000US-0597707.  
PR 14-JUL-2000; 2000US-0616807.  
PR 19-SEP-2000; 2000US-0664641.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YF, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
PI Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;  
PI Dirmanac R;  
XX  
XX WPI: 2001-589862/66.  
DR N-PSDB: AAS44597.  
XX  
XX Novel polypeptides and nucleic acids obtained from cDNA libraries  
PT prepared from various human tissues, for diagnosis, treatment of  
PT cancer, neurological, inflammatory disorders and for use in arrays for  
PT detection -  
XX  
XX Claim 10; SEQ ID NO 194; 153pp; English.  
PS  
XX  
XX Sequences AAU27676-AAU28019 represent full-length polypeptides and  
CC contig polypeptides of the invention. The proteins and their associated  
CC DNA sequences are useful for the treatment, diagnosis and prevention of  
CC various types of disorder in a mammalian subject such as a human, dog,  
CC monkey, mouse, hamster or rat. The disorders include cancers such as  
CC leukaemia, lymphoma and neuroblastoma, autoimmune disorders such as  
CC multiple sclerosis, connective tissue disease, rheumatoid arthritis,  
CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system  
CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's  
CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and  
CC Werner's disease, inflammatory disorders such as nephritis, Crohn's  
CC disease, ischemia-reperfusion injury, shock, sepsis and inflammatory  
CC bowel disease. The sequences exhibit activity relating to angiogenesis,  
CC cell proliferation, cell differentiation, stem cell growth factor,  
CC activin or inhibin. Therefore, they can be used to manipulate stem cells  
CC in culture to give rise to neuroepithelial cells that can be used to  
CC augment or replace cells damaged by illness, accidental damage or genetic  
CC disorders. The sequences may also be used for regeneration of bone,  
CC cartilage, tendons and ligaments and in tissue repair and burn healing.  
CC Note: Some sequences for this patent did not form part of the printed  
CC specification, but were obtained in electronic format directly from WIRO  
CC at ftp.wipo.int/pub/published\_pcl\_sequences.  
XX  
XX  
SQ Sequence 471 AA;

Query Match 62.6%; Score 1552.5; DB 22; Length 471;  
Best Local Similarity 61.5%; Pred. No. 2.3e-133;

Matches	286; Conservative	85; Mismatches	87; Indels	7; Gaps	2;
OY	17	DAEPTRETEFLDALDRNGDGVNDIGELQEGIRNIGLIGD----	ABEKIFTTGDVVKD	72	
Db	7	daerrtqwgriifeeldsnkdgrvdvhelrvgjarlg---ggnpdpqaqgissegdaddp	63		
OY	73	GKLDPEEFMYLKDHEKKMKLAFKSLDKNNDKITIASETVSLQTLGITISEQOAEIILQ	132		
Db	64	ggldeefsyrlgereqlllmfnsldrngqhdvseiqsfalagisilegaeikllh	123		
OY	133	SIDVDGWTVDWNEWRDYFLFNPVTDEIIRFKMHSSTGIDIGSLTIPDEFTDEKKS	192		
Db	124	smrdgtmldwgewrdfhlhslenvedvlyfwkhsfvldlgecltyvpefdefskqekltg	183		
OY	193	QMWROLLAGGIAGAVSRSTAPLRKTIIMQVHSGSKDKMIFGGRQVMVEGGRISLR	252		
Db	184	mwqglvavagavavstgtctapdrllvfmqvhasktmrlllgllsmvleggylrstwr	243		
OY	253	GNGTNVIRIAPETAVKFWAYEORYKKLITEEGOKIGTERFISGSAGATAOTFTYPM	312		
Db	244	gnglnvklipesaiklmayeqikrallggqetlhvgerfvaagslagataqtlilypmev	303		
OY	313	KTRIAVGKTGYSGIYDCAKKILKHEGLGAFYKGYVNPGLGITPYAGIDLAAYELL	372		
Db	304	ktlrlttrtgqykglllccarrlleregrpratyglpvnlgldlyagldlavetclkmw	363		
OY	373	LDNFAKDSVNGVWVLGGCLSTGCLASYPALVTRTMOAAMLEGSPOLMWGIFR	432		
Db	364	lqgshsadsdpgllvlllaqclstscqglasypalvtrtmqadaslegpqqlsmgltr	423		
OY	433	RIISKEGIPGLYRGITPNFMKVLPAVGISYVVENMKOTLGVTOK	477		
Db	424	hlisqegmrglyrgitapnfmkvlpavalsiyvvenmkqalgvtar	468		
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ID	AAU27869	standard; Protein: 509 AA.			
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AC	XX				
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DT	18-DEC-2001	(first entry)			
XX	XX				
DE	Human contig polypeptide sequence #22.				
XX	XX				
KW	Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;				
KW	mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;				
KW	cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;				
KW	nervous system disorder; inflammatory disorder; cell differentiation;				
KW	angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;				
KW	genetic disorder; bone regeneration; tendon; ligament; tissue repair;				
KW	cytostatic; antineoplastic; antiproliferative; vulnery; antiinflammatory;				
KW	antibacterial; immunosuppressive; vasotropic; antiparkinsonian;				
KW	neuroprotective; osteopathic; antidiabetic; antiashtmatic; antiallergic;				
KW	immunostimulant; analgesic; gene therapy.				
XX	XX				
OS	Homo sapiens.				
OS	Synthetic.				
XX	XX				
PN	WO200164834-A2.				
XX	XX				
PD	07-SEP-2001.				
XX	XX				
PF	26-FEB-2001; 2001WO-US04926.				
XX	XX				
PR	28-FEB-2000; 2000US-0515126.				
PR	18-MAY-2000; 2000US-0577409.				
PR	17-JUN-2000; 2000US-0597707.				
PR	14-JUL-2000; 2000US-0616807.				
PR	19-SEP-2000; 2000US-0664641.				
XX	XX				
PA	(HYSE-) HYSEQ INC.				

PI	Tang YF, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;				
PI	Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;				
PI	Drmanic R;				
DR	WPI: 2001-589862/66.				
XX	N-PSDB: NAA44769.				
XX					
PT	Novel polypeptides and nucleic acids obtained from cDNA libraries				
PT	prepared from various human tissues, for diagnosis, treatment of				
PT	cancer, neurological, inflammatory disorders and for use in arrays for				
PT	detection				
PS	Claim 10; Page 126-127; 153pp; English.				
XX	XX				
CC	Sequences AAU27676-AAU28019 represent full-length polypeptides and				
CC	contig polypeptides of the invention. The proteins and their associated				
CC	DNA sequences are useful for the treatment, diagnosis and prevention of				
CC	various types of disorder in a mammalian subject such as a human, dog,				
CC	monkey, mouse, hamster or rat. The disorders include cancers such as				
CC	leukaemia, lymphoma and neuroblastoma, autoimmune disorders such as				
CC	multiple sclerosis, connective tissue disease, rheumatoid arthritis,				
CC	diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system				
CC	disorders such as Parkinson's disease, Alzheimer's disease, Huntington's				
CC	chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and				
CC	Wernicke disease, inflammatory disorders such as nephritis, Crohn's				
CC	disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory				
CC	bowel disease. The sequences exhibit activity relating to angiogenesis,				
CC	cell proliferation, cell differentiation, stem cell growth factor,				
CC	activin or inhibin. Therefore, they can be used to manipulate stem cells				
CC	in culture to give rise to neuroepithelial cells that can be used to				
CC	augment or replace cells damaged by illness, accidental damage or genetic				
CC	disorders. The sequences may also be used for regeneration of bone,				
CC	cartilage, tendons and ligaments and in tissue repair and burn healing.				
CC	Note: Some sequences for this patent did not form part of the printed				
CC	specification, but were obtained in electronic format directly from WIPO				
CC	at ftp.wipo.int/pub/published_pcl_sequences.				
XX	XX				
SO	Sequence 509 AA;				
Query Match	62.6%; Score 1552.5; DB 22; Length 509;				
Best Local Similarity	61.5%; Pred. No. 2.6e-133;				
Matches	286; Conservative 85; Mismatches 87; Indels 7; Gaps 2;				
OY	17	DAEPTRETEFLDALDRNGDGVNDIGELQEGIRNIGLIGD----	ABEKIFTTGDVVKD	72	
Db	45	daerrtqwgriifeeldsnkdgrvdvhelrvgjarlg---ggnpdpqaqgissegdaddp	101		
OY	73	GKLDPEEFMYLKDHEKKMKLAFKSLDKNNDKITIASETVSLQTLGITISEQOAEIILQ	132		
Db	102	ggldeefsyrlgereqlllmfnsldrngqhdvseiqsfalagisilegaeikllh	161		
OY	133	SIDVDGWTVDWNEWRDYFLFNPVTDEIIRFKMHSSTGIDIGSLTIPDEFTDEKKS	192		
Db	162	smrdgtmldwgewrdfhlhslenvedvlyfwkhsfvldlgecltyvpefdefskqekltg	221		
OY	193	QMWROLLAGGIAGAVSRSTAPLRKTIIMQVHSGSKDKMIFGGRQVMVEGGRISLR	252		
Db	222	mwqglvavagavavstgtctapdrllvfmqvhasktmrlllgllsmvleggylrstwr	281		
OY	253	GNGTNVIRIAPETAVKFWAYEORYKKLITEEGOKIGTERFISGSAGATAOTFTYPM	312		
Db	282	gnglnvklipesaiklmayeqikrallggqetlhvgerfvaagslagataqtlilypmev	341		
OY	313	KTRIAVGKTGYSGIYDCAKKILKHEGLGAFYKGYVNPGLGITPYAGIDLAAYELL	372		
Db	342	ktlrlttrtgqykglllccarrlleregrpratyglpvnlgldlyagldlavetclkmw	401		
OY	373	LDNFAKDSVNGVWVLGGCLSTGCLASYPALVTRTMOAAMLEGSPOLMWGIFR	432		
Db	402	lqgshsadsdpgllvlllaqclstscqglasypalvtrtmqadaslegpqqlsmgltr	461		
OY	433	RIISKEGIPGLYRGITPNFMKVLPAVGISYVVENMKOTLGVTOK	477		

Db	462	hlsqegmrglyrgiapnfmkxlpavsisyvyemkqalgvtlr	506
RESULT	4		
ID	AAV6718		
XX	AAV6718 standard; protein; 469 AA.		
XX			
AC	AAV6718;		
XX			
DT	05-APR-2000 (first entry)		
XX			
DE	Membrane-bound protein PRO1106.		
XX			
KW	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;		
KX	pharmaceutical; receptor immunoadhesin; gene mapping.		
XX			
OS	Homo sapiens.		
XX			
PN	W0963088-A2.		
XX			
PD	09-DEC-1999.		
XX			
PF	02-JUN-1999; 99WO-US12252.		
XX			
02-JUN-1998;	98US-0087607.		
02-JUN-1998;	98US-0087609.		
02-JUN-1998;	98US-0087759.		
03-JUN-1998;	98US-0087827.		
04-JUN-1998;	98US-0088021.		
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05-JUN-1998;	98US-0088167.		
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09-JUN-1998;	98US-0088655.		
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19-JUN-1998;	98US-0089947.		
19-JUN-1998;	98US-0089948.		

PR	13-JUN-1998	98US-00989542
PR	22-JUN-1998	98US-00989245
PR	22-JUN-1998	98US-00987352
PR	22-JUN-1998	98US-00987045
PR	23-JUN-1998	98US-00980349
PR	23-JUN-1998	98US-00980355
PR	24-JUN-1998	98US-00980425
PR	24-JUN-1998	98US-00980431
PR	24-JUN-1998	98US-00980435
PR	24-JUN-1998	98US-00980444
PR	24-JUN-1998	98US-00980461
PR	24-JUN-1998	98US-00980472
PR	24-JUN-1998	98US-00980535
PR	25-JUN-1998	98US-00980688
PR	25-JUN-1998	98US-00980691
PR	25-JUN-1998	98US-00980694
PR	25-JUN-1998	98US-00980695
PR	25-JUN-1998	98US-00980696
PR	26-JUN-1998	98US-00980662
PR	26-JUN-1998	98US-00980683
PR	01-JUL-1998	98US-00981358
PR	01-JUL-1998	98US-00981360
PR	01-JUL-1998	98US-00981544
PR	02-JUL-1998	98US-00981478
PR	02-JUL-1998	98US-00981486
PR	02-JUL-1998	98US-00981519
PR	02-JUL-1998	98US-00981562
PR	02-JUL-1998	98US-00981628
PR	02-JUL-1998	98US-00981633
PR	02-JUL-1998	98US-00981646
PR	02-JUL-1998	98US-00981673
PR	07-JUL-1998	98US-00981982
PR	07-JUL-1998	98US-00981987
PR	09-JUL-1998	98US-00982182
PR	10-JUL-1998	98US-00983339
PR	30-JUL-1998	98US-00984651
PR	04-AUG-1998	98US-00985282
PR	04-AUG-1998	98US-00985285
PR	04-AUG-1998	98US-00985301
PR	04-AUG-1998	98US-00985302
PR	04-AUG-1998	98US-00985318
PR	04-AUG-1998	98US-00985321
PR	10-AUG-1998	98US-00985325
PR	10-AUG-1998	98US-00985329
PR	10-AUG-1998	98US-00986102
PR	11-AUG-1998	98US-00986143
PR	11-AUG-1998	98US-00986146
PR	12-AUG-1998	98US-00986329
PR	17-AUG-1998	98US-00986757
PR	17-AUG-1998	98US-00986768
PR	17-AUG-1998	98US-00986773
PR	17-AUG-1998	98US-00986971
PR	17-AUG-1998	98US-00986967
PR	17-AUG-1998	98US-00986981
PR	17-AUG-1998	98US-00986994
PR	17-AUG-1998	98US-00986995
PR	17-AUG-1998	98US-00986997
PR	18-AUG-1998	98US-00986949
PR	18-AUG-1998	98US-00986950
PR	18-AUG-1998	98US-00986956
PR	18-AUG-1998	98US-00986960
PR	18-AUG-1998	98US-00987411







XX 27-MAR-2000 (first entry)  
DE Murine ADR/ATP transporter family protein, SEQ ID NO:339.  
KW Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;  
KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell;  
KW secreted; transmembrane; inflammation; cancer; neurological disease;  
KW angiogenesis; tumour vascularisation; growth disorder;  
KW developmental disorder; skin wound; hair follicle disorder;  
KW anti-inflammatory; cytostatic; neuroprotective; vulnery.  
XX  
XX Mus sp.  
XX WO955865-A1.  
XX 04-NOV-1999.  
XX 29-APR-1999; 99WO-NZ00051.  
XX 29-APR-1998; 98US-0069726.  
XX 09-NOV-1998; 98US-0188930.  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
XX Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murlison JG;  
XX WPI: 2000-072177/06.  
XX N-PSDB: AA61789.  
XX Novel polynucleotides useful for the treatment of various conditions  
XX including wounds and cancer -  
XX  
XX Claim 4; Page 199-200; 235pp; English.  
XX  
XX The invention relates to novel nucleic acid sequences derived from rat  
XX dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,  
XX and mouse embryonic skin, keratinocyte stem cells and transit amplifying  
XX cells. Polypeptides of the invention may be used to treat inflammation,  
XX cancer and neurological diseases. The proteins may be used to stimulate  
XX the growth and motility of keratinocytes, to inhibit the growth of  
XX cancer cells, to modulate angiogenesis and tumour vascularisation, to  
XX inhibit skin inflammation, to modulate epithelial cell growth and to  
XX inhibit binding of HIV-1 to leukocytes. The invention may also be used  
XX to treat growth and developmental defects, skin wounds and hair follicle  
XX disorders. Sequences AA75942-Y76123 represent polypeptides encoded  
XX by cDNA sequences derived from several mouse, rat or human skin cell  
XX types. Sequences AA75942-Y75947, AA76020-Y76021, AA76094-Y76104 and  
XX AA76119 are proteins with an N-terminal signal sequence, indicating  
XX that they are secreted. Sequences AA75986-Y75989, AA76061-Y76071,  
XX AA76106-Y76109 and AA76121-Y76122 are proteins with one or more  
XX putative transmembrane domains.  
XX  
XX Sequence 469 AA:  
SQ

Query Match 60.4%; Score 1499; DB 21; Length 469;  
Best Local Similarity 65.6%; Pred. No. 1.8e-128;  
Matches 274; Conservative 73; Mismatches 71; Indels 0; Gaps 0;

QY 60 EKIIFTTGDNVNDKGLDFEFEMKYLKDHEKMKLAFLSKDNNDGKTEASEIVSIQTIG 119  
DB 52 kqklvgaqgkldldgldfvdhkydqheklrlrvksldkndgldgeqlmsldrdy 111  
QY 120 LTISSQQAALLIQTSDIVDSTMTVDNNEKRDYFLFNPVYTIIEELIRWKSTGIDIDSLT 179  
DB 112 vrlseqgaekllksmckngltmldwnewrdyhlhlpvenihellywkhstlfdvgent 171

QY 180 IPDEFTEDEKSGGOMWROLLAGIAGAVASTAPLRLKIMMVGKSGDKMNINGGR 239  
DB 172 vpdelfteerqgwmwrhlvvaaggagavsrctclapldrlkvlmqvnaasnmncivgfl 231  
QY 240 OMVKBGGIRSLMRNGTGNVIAETAVKFWAYEYKLLTEEGOKIGTFERFISGMAG 299

DB 232 qmlreggaksllwrgnglnvklkipesaklkmaygqmrlvgsdgelrlherlvagslag 291  
QY 300 ATAQTFIYPMWEWMAKTRILAVKCTGOYSGIYDCAKILKHEGIGAFYKATVPNLGIIPYAG 359  
DB 292 alqsgslpmevklktrmalrlktgysgmlcdarrllakegvaelykylpmlglipyag 351  
QY 360 IDLAVVELLSYMLDNPFAKSVNPGVWVLLGCGALSTCGOLASYPALVTRWQAQAML 419  
DB 352 ldlavvelkntwldqryavnsadpgvrvllacgllstcgqlasypalvtrwqaqasi 411  
QY 420 EGSPOLMNVGLFRRIISKEGIPGLYRGITPEFMKVLPAVGIISVYVNEKMTGIGVTK 477  
DB 412 egapevumsslfrqglrtgagafglyrslapnfmkvlpavsisyvvynlklitlgvqr 469

RESULT 8  
AAB56023  
ID AAB56023 standard; Protein; 469 AA.  
XX  
XX AAB56023;  
AC  
XX 08-MAR-2001 (first entry)  
DT  
XX Skin cell protein, SEQ ID NO: 339.  
DE  
XX  
XX Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV;  
KW nootropic; neuroprotective; vulnery; immunomodulatory; vaccine;  
KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;  
KW inflammation; neurological disease.  
XX  
XX Mus sp.  
OS  
XX  
XX WO200069884-A2.  
XX  
XX 23-NOV-2000.  
PD  
XX  
XX 15-MAY-2000; 2000WO-NZ00075.  
PF  
XX  
XX 14-MAY-1999; 99US-0312283.  
PR  
XX  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
PA  
XX  
PI Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murlison JG;  
XX WPI: 2001-007495/01.  
DR N-PSDB: AAC99722, AAC99806.  
XX  
XX New isolated polynucleotide used in the identification of genetic  
XX disorders and encoding polypeptides used for treating inflammatory  
XX disease, cancer and neurological diseases -  
XX  
XX Claim 4; Page 266-267; 352pp; English.  
XX  
XX The present sequence is a polypeptide which is expressed in  
XX mammalian skin cells. The polypeptide is useful for stimulating  
XX keratinocyte growth and motility, inhibiting the growth of cancer cells,  
XX modulating angiogenesis, inhibiting angiogenesis and vascularisation of  
XX tumours, modulating skin inflammation, stimulating the growth of  
XX epithelial cells, inhibiting the binding of human immunodeficiency virus  
XX (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and  
XX neurological diseases. The polynucleotide can be used as a marker, in  
XX the identification of genetic disorders, and for the design of  
XX oligonucleotides for examining expression patterns.  
XX  
XX Sequence 469 AA:  
SQ

Query Match 60.4%; Score 1499; DB 22; Length 469;  
Best Local Similarity 65.6%; Pred. No. 1.8e-128;  
Matches 274; Conservative 73; Mismatches 71; Indels 0; Gaps 0;

QY 60 EKIIFTTGDNVNDKGLDFEFEMKYLKDHEKMKLAFLSKDNNDGKTEASEIVSIQTIG 119

DB 52 kqkivagqdkaldgldfeefvhyiqdhekkirlyfksldkndgridageimgslrdlg 111  
QY 120 LTISSQOAEILLIQSIDVOSTMTVDNENMDYFLFNPVDIEELIFPKHSTGIDIGDSLT 179  
DB 112 vliisqgaekllksmdkngtumlidmewrdyhlhnpvenlillywksltfdvgentl 171  
QY 180 IPDEFTEDEKSSGOWMROLIAGIAGAVSRSTAPLDRILKIMQVHSGSKSDKMNIFGGR 239  
DB 172 vdfeltveerqgmwvrlhvaggagavsrctctapldrlkvlmqvhasrsmnmcivgftl 231  
QY 240 OMVKGSGIRSLRNGNTNVIKTAPEYAVKFMAYEORYKLLTEGOKIGTFEFGSGNAG 299  
DB 232 qmrlrggaksrlwrgnglnvklkapesalklmageqmkrlvgsdqetlrlherlvagslag 291  
QY 300 ATAOFETVPMEMKTRFLAVGKTGOYSGIYDCAKIKILKHEGLAFKGYVNPNLGITIPYAG 359  
DB 292 alagsslypmeylklrmlarktcqysgmldcarrllakegvaafkkyaplmhglilpyag 351  
QY 360 IDLAVYELIKSYWLDNFADSVNPGVMVLLGCGALSTGQGLASYPALVTRTMOAOAML 419  
DB 352 ldlavyetlknwlgryavnsadpgvflaacgtlssctgqlasypalvtrtmqagast 411  
QY 420 EESPOLNMVGLFRRITISKEGIPGLYRGITPNPMKVLPAVGISYVYVENMKOTLGYTOK 477  
DB 412 egapevtmslftkqllrlegafglyrjlapnfmkvipavslsyvvyenmkltclgyvqr 469

RESULT 9  
ABG22637  
ID ABG22637 standard; Protein; 508 AA.  
XX AC ABG22637;  
XX DT 18-FEB-2002 (first entry)  
XX DE Novel human diagnostic protein #22628.  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX OS Homo sapiens.  
PN WO200175067-A2.  
XX PD 11-OCT-2001.  
XX PE 30-MAR-2001; 2001WO-US08631.  
XX PR 31-MAR-2000; 2000US-0540217.  
XX PR 23-AUG-2000; 2000US-0649167.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Dmanac RT, Liu C, Tang YT;  
XX DR WPI; 2001-639362/73.  
XX DR N-PSDB; AAS86824.  
XX PT New isolated polynucleotide and encoded polypeptides, useful in  
XX PT diagnostics, forensics, gene mapping, identification of mutations  
XX PT responsible for genetic disorders or other traits and to assess  
XX PT biodiversity  
XX PS Claim 20; SEQ ID NO 52996; 103pp; English.

The invention relates to isolated polynucleotide (I) and  
polypeptide (II) sequences. (I) is useful as hybridisation probes,  
polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
and gene mapping, and in recombinant production of (II). The  
polynucleotides are also used in diagnostics as expressed sequence tags  
for identifying expressed genes. (I) is useful in gene therapy techniques  
to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pcl\_sequences.  
XX SQ Sequence 508 AA;

Query Match 59.6%; Score 1479.5; DB 22; Length 508;  
Best Local Similarity 59.3%; Pred. No. 1.3e-126;  
Matches 277; Conservative 85; Mismatches 96; Indels 9; Gaps 4;

QY 17 DAEQFRTYETLQALDRNDSGVVDIGELQEGRLNIGLPGOD---AEEKRTTGDVKD 72  
DB 45 deerrqqrgrlleeidsnkdgrvdvdelrqlarlg---ggnpdpqagqgssegdapn 101  
QY 73 GKLDPEEFKMYLKDHEKKMKLAFKSLDKNNDKIRASEIVQSLQTLGTLISQOAEI-IL 131  
DB 102 gldldeefsfrylqereqrlmlfhdldrngdhlvselqgsfralgslllegckhfa 161  
QY 132 QSIDVDGTWTVDNENMDYFLFNPVDIEELIRFKHSTGIDIGSLTIPDEFTEDEKS 191  
DB 162 gavdrqgmldwgewrdfllhslenvedvlyfkhsatvldigcelvtpdefskqeklt 221  
QY 192 GQWNRQLLAGIAGAVSRSTAPLDRILKIMQVHSGSKSDKMNIFGFGQMWVEGIRSLW 251  
DB 222 gmwvkkqagavagavsrstgvpldrlkvmqvhasknrlngllsmyvggslrslw 281  
QY 252 RQNGTNNVIKTAPEYAVKFMAYEORYKLLTEGOKIGTFEFGSGMAGATAOTFYTMEV 311  
DB 282 rgnjnlvklkapesalklmageqikralpgeketlrvlerfagslagatcllylpmev 341  
QY 312 MKTRLAVGKTGOYSGIYDCAK-KILKHGCLAFYGYVNPNLGITIPYAGIDLAVYELKS 370  
DB 342 lktlrltrtgqykglaqlrgrllereqprafyglpvnvlgldlavyetlkn 401  
QY 371 VWLDNFADSVNPGVMVLLGCGALSTGQGLASYPALVTRTMOAOAMEGSPOLNMVGL 430  
DB 402 wllqgysndsadpgllvlacgtlssctgqlasypalvtrtmqagastlegqklsmlyl 461  
QY 431 FRRITISKEGIPGLYRGITPNPMKVLPAVGISYVYVENMKOTLGYTOK 477  
DB 462 lrlhlsqegmrglyrjlapnfmkvipavslsyvvyenmkqalgvtsr 508

RESULT 10  
AAB42329  
ID AAB42329 standard; Protein; 385 AA.  
XX AC AAB42329;  
XX DT 08-FEB-2001 (first entry)  
XX DE Human ORFX ORF2093 polypeptide sequence SEQ ID NO:4186.  
XX KM Human; open reading frame; ORFX; detection; cytosstatic; hepatotropic;  
XX KM vulnereary; antiporiatric; antiparkinsonlan; nootropic; neuroprotective;  
XX KM anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
XX KM immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
XX KM hypotensive; dermatological; immunosuppressive; antiinflammatory;  
XX KM antiviral; antibacterial; antifungal; antihematic; antihyroid;  
XX KM antianemic; gene therapy; cancer; proliferative disorder; hypertension;  
XX KM neurodegenerative disorder; osteoarthritis; graft vs host disease;





[illegible]

PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-488781/53.  
DR N-PSDB; AA163830.  
XX  
XX New isolated nucleic acids and polypeptides, useful for diagnosing,  
PT treating and/or preventing human diseases and disorders -  
XX  
XX Claim 11; SEQ ID NO 202; 664pp + Sequence Listing; English.  
XX  
XX The invention relates to human polynucleotides (AA163803-AA164012) and  
CC the encoded proteins (AA1643497-AA1643660) useful for preventing, treating  
CC or ameliorating medical conditions e.g. by protein or gene therapy. The  
CC genes were isolated from a range of human tissues disclosed in the  
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists  
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,  
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,  
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or  
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,  
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,  
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
CC and parasitic infections.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pctl\_sequences.  
XX  
XX  
SQ Sequence 244 AA:

Query Match 46.1%; Score 1143; DB 22; Length 244;  
Best Local Similarity 94.8%; Pred. No. 2.7e-96;  
Matches 219; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 MRLMLRDLPLPTAACDAQAPRTRETLFQALDRNGGVVDIGELGGLNLTGIPICGDAE 60  
DB 14 MLRLVIRDFVLPACXQDAEQPTRETLFQALDRNGGVVDIGELGGLNLTGIPICGDAE 73  
OY 61 EKIFTTGVDNRKQGLDPEEFEMKYLKDKHEKKMLAFKSLDKNNDKTEASEIYOSLTGL 120  
DB 74 EKIFTTGVDNRKQGLDPEEFEMKYLKDKHEKKMLAFKSLDKNNDKTEASEIYVSGTGL 133

OY 121 TISEQAEILLIISIDVDGTMVDMNEMWRDYFLFNPTVDIEIIRKKNSTGIDIGSLTI 180  
DB 134 TLSEGGAEILLIISIDVDGTMVDMNEMWRDYFLFNPTVDIEIIRKKNSTGIDIGSLTI 193  
OY 181 PDFFTEDEKSSGQWWRQLLAGIAGVSRTPAPIDRLKIMMVOHGSKSDK 231  
DB 194 pdfftedekssgqwwrqlilagigagaxstspidrlkimvgvgnqtk 244  
RESULT 14  
AA19941  
ID AA19941 standard; Protein; 244 AA.  
XX  
XX AA19941;  
AC  
XX  
DT  
XX  
XX 06-DEC-2001 (first entry)  
DE Novel human calcium-binding protein #50.  
XX  
XX Human; calcium-binding protein; calcium flux; neurological disease;  
KW immune dysfunction; digestive disorder; neoplastic disease;  
KW blood disorder; infectious disease; gene therapy; immunosuppressive;  
KW antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;  
KW virucide.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO20015304-A2.  
PN  
XX  
PD 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US01302.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 04-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.



PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234423.  
PR 21-SEP-2000; 2000US-0234424.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239335.  
PR 13-OCT-2000; 2000US-0239337.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.

PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PI Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-465568/50.  
DR N-PSDB; AAS31626.  
XX  
PT Isolated nucleic acid molecule encoding a calcium-binding protein is  
XX used in preventing, treating or ameliorating a medical condition -  
PS Claim 11; SEQ ID No 138; 542pp; English.  
XX  
XX The present invention relates to the isolation of novel human  
CC calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic  
CC sequences encoding for these proteins. The sequences of the invention  
CC are useful in the diagnosis, prevention and/or prognosis of diseases  
CC associated with aberrant calcium flux. Such disorders include  
CC neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),  
CC immune dysfunction (e.g. severe combined immunodeficiency, SCID),  
CC digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic  
CC disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or  
CC infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The  
CC novel calcium-binding proteins are also useful as screening tools to  
CC identify antagonists and/or agonists that may enhance or inhibit  
CC activities mediated by calcium-binding proteins. The polynucleotides of  
CC the invention are also useful in gene therapy. AAU19892-AAU19969  
CC represent the novel human calcium-binding proteins.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences.  
SQ Sequence 244 AA:  
  
Query Match 46.1%; Score 1143; DB 22; Length 244;  
Best local similarity 94.8%; Pred. No. 2,7e-96;  
Matches 219; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
  
QY 1 MRLWRLDFALPTAACDAPRTYETLFQALDRNGDVVVGIGELGRNLGPIGDAAE 60  
DB 14 MLTWLRFDFVLPtaxcqaesprtyetlfgaldtngdvvgvlgelqegllnlp19gdae 73  
QY 61 EKIFTTGDVANKDKLDFFEEPMKYLKDHEKKMLAFKSLDRNNNGKIASETVOSLQTLGL 120  
DB 74 ekifftgdvankdglDteetmkyLkdhckmklafksldknnngkiasetvsglqlgl 133  
QY 121 TISEQQAELILQSIDVDGNTFTVDNEMKRDYFLPNPVTDEIIRFKWHSRGIDIGSLTT 180  
DB 134 tiseqqaellilqsidvgtntcxdwnewrdyflfnpvxtdeeilrfwhtsgldigsdltl 193

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Oy      181 PDEFTEDEKSSGQWWRQLLAGGIAGAVSRTSTAPLDRKLIMQVHGSKSDk   231  
         |||||  
Db      194 pdeftedekssgqwrqlaggiagaaxststgpldrklmmvgtcgntck    244
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RESULT 15  
ADDE0300

ID AAB50388 standard; Protein; 292 AA.

AC AAB50388;

DT 12-MAR-2001 (first entry)

DE Human uncoupling protein #11.

KM Human; uncoupling protein; immunosuppressive; antiarthritic;  
KM antineumatic; antiproliferative; cardiac; vasotropic;  
KM cerebroprotective; neuroprotective, antibacterial; ophthalmological;  
KM gastrointestinal; nephrotoxic; gynaecological; vulnary; thrombolytic;  
KM gene therapy; cancer; wound; infectious disease; thrombosis; arthritis;  
KM infertility.

05 Homo sapiens.

PN WO2000061614-A2.

PD 19-OCT-2000.

PF 06-APR-2000; 2000WO-US09534.

PR 09-APR-1999; 99US-0128701.

PR 08-JUL-1999; 99US-0142821.

PR	18-AUG-1999;	99US-0149448.
PR	13-NOV-1999;	99US-0154751.

PK 12-NOV-1999; 9905-01064/51L  
XX

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Ni J, Komatsoulis G, Rosen CA, Soppet DR:

WPI: 2000-656322/63.

DR N-PSDB; AAC90462.

PT Uncoupling proteins and nucleic acid sequences encoding them, useful  
PT for detecting, preventing and treating proliferative, neurological,  
PT immune system, cardiovascular and gastrointestinal disorders -

PS Claim 11; Page 328-329; 343pp; English.

CC The present sequence is a human uncoupling protein. The nucleotide

CC sequences encoding the uncoupling proteins may be used for

the detection of various disorders such as cancer, for chromosome identification, for chromosome markers and for numerous other diagnostic

or research purposes. The uncoupling protein encoded by the nucleotide CC identifies some chromosomes and for numerous other diagnostic

sequences may be used to treat disorders such as neural, immune, or research purposes; the uncoupling protein encoded by the nuclear

muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,

CC renal and proliferative disorders, wounds, infectious diseases,

CC thrombosis, arthritis, and infertility.

50 Sequence 292 AA;

Query match 41.88; Score 1037; DB 21; Length 292;

Matches 181; Conservative 53; Mismatches 44; Indels 0; Gaps 0;

.....

140 MTVDWNEWRDYFLFNPVTDIEEIRFWKHSTGIDIGDSLTIPEFTEDEKKSQWWRQL 1999

1 mti ducur d h f i l h a j o v r o d u j u f e l k b a t u j d i a o o j t u n d o f e k c o k j t a e w t i c j r e n

QY 200 AGGIAGAVSRTSTAPLDRLKIMQVHGSKSDKMNIFGGFRQWKEGGIRSLWRGNGTNI 259

Db 61 agavagavsr t g t a p l d r l k v f m q v h a s k t n r l n l g l r s m v l e g g i r s l w r g n g i n v l 120

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Qy 260 KIAETA VKWAEYEDYKKLLEEGÖKIGTFERISGSMA GATAOFTIYPEVWKTRLAVG 319
      |||||::|| ||| : :: : ||:::||:||||| |||||:||||| :
Db 121 kiapesaikmayeqikraliygqetihvgerfvagslagataqilijymevlkitrltlr 180
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QY 320 KTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLSYWLDFAKD 379

Db 181 rtgqykgllldcarrlleregprafyrqylpnvlgilpyagidlavyetlknwllqyshd 240

QY 380 SVNPGVMVLGGGALSSTCGQLASYPLALVTRMQAQA 417

Db 241 sadpgilvllacgtistcglasyplalvrtrmqqa 278

Search completed: August 18, 2002, 09:22:20  
Job time: 3814 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2002, 08:14:06 ; Search time 24.71 Seconds  
(without alignments)  
471.510 Million cell updates/sec

Title: US-09-777-921A-2  
2481  
Sequence: 1 MLRWLRDFALEPTACQDAEQ.....VGISYVYENKQRTLGVTOK 477

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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5: /cgn2\_6/ptodata/1/1aa/PTCUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Dackfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1499	60.4	469	US-09-188-930-339	Sequence 339, App
2	910	36.7	312	US-09-188-930-142	Sequence 142, App
3	347	14.0	298	US-08-961-871-10	Sequence 10, Appl
4	323.5	13.0	328	US-09-068-140A-15	Sequence 15, Appl
5	311.5	12.6	289	US-09-068-140A-10	Sequence 10, Appl
6	295	11.9	320	US-08-933-750C-12	Sequence 12, Appl
7	295	11.9	320	US-09-234-613-12	Sequence 12, Appl
8	281	11.3	674	US-09-160-119-2	Sequence 12, Appl
9	269.5	10.9	447	US-09-160-119-4	Sequence 2, Appl
10	255	10.3	351	US-08-933-750C-19	Sequence 19, Appl
11	255	10.3	351	US-09-234-613-19	Sequence 19, Appl
12	239.5	9.7	311	US-08-775-009-33	Sequence 32, Appl
13	233.5	9.4	299	US-08-518-878B-56	Sequence 56, Appl
14	233.5	9.4	299	US-08-470-868A-56	Sequence 56, Appl
15	233.5	9.4	309	US-08-518-878B-51	Sequence 51, Appl
16	233.5	9.4	309	US-08-807-861A-51	Sequence 51, Appl
17	233.5	9.4	309	US-08-470-868A-51	Sequence 51, Appl
18	233.5	9.4	309	US-09-210-681-51	Sequence 51, Appl
19	233.5	9.4	309	US-08-946-719A-51	Sequence 51, Appl
20	233.5	9.4	311	US-08-775-009-33	Sequence 51, Appl
21	229	9.2	312	US-09-142-565-2	Sequence 33, Appl
22	228	9.2	432	US-08-937-466-4	Sequence 4, Appl
23	228	9.2	432	US-09-172-528-4	Sequence 4, Appl
24	228	9.2	432	US-09-318-199-4	Sequence 4, Appl
25	228	9.2	432	US-09-503-579-4	Sequence 4, Appl
26	226	9.1	306	PCT-US94-09799-1	Sequence 1, Appl
27	224	9.0	308	US-08-937-466-2	Sequence 2, Appl

28	224	9.0	308	US-09-172-528-2	Sequence 2, Appl
29	224	9.0	308	US-09-318-199-2	Sequence 2, Appl
30	224	9.0	308	US-09-503-579-2	Sequence 2, Appl
31	198.5	8.0	303	US-08-518-878B-37	Sequence 37, Appl
32	198.5	8.0	303	US-08-294-522B-36	Sequence 36, Appl
33	198.5	8.0	303	US-08-807-861A-37	Sequence 37, Appl
34	198.5	8.0	303	US-08-470-868A-37	Sequence 37, Appl
35	198.5	8.0	303	US-09-210-681-37	Sequence 37, Appl
36	198.5	8.0	303	US-08-946-719A-37	Sequence 37, Appl
37	193.5	7.8	307	US-08-807-861A-56	Sequence 56, Appl
38	193.5	7.8	307	US-09-210-681-56	Sequence 56, Appl
39	193.5	7.8	307	US-08-946-719A-56	Sequence 56, Appl
40	186	7.5	125	US-08-905-223-320	Sequence 320, App
41	179	7.2	256	US-08-937-466-6	Sequence 6, Appl
42	179	7.2	256	US-09-172-528-6	Sequence 6, Appl
43	179	7.2	256	US-09-318-199-6	Sequence 6, Appl
44	179	7.2	256	US-09-503-579-6	Sequence 6, Appl
45	178	7.2	149	US-08-100-874-2	Sequence 2, Appl

## ALIGNMENTS

```
RESULT 1
US-09-188-930-339
: Sequence 339, Application US/09188930A
: Patent No. 6150502
:
: GENERAL INFORMATION:
: APPLICANT: Watson, James D.
: APPLICANT: Strachan, Lorna
: APPLICANT: Sleeman, Matthew
: APPLICANT: Onrust, Rene
: APPLICANT: Morrison, James Greg
:
: TITLE OF INVENTION: Compositions Isolated From Skin Cells
: FILE REFERENCE: 11000.1011c1
: CURRENT APPLICATION NUMBER: US/09/188,930A
: NUMBER OF SEQ ID NOS: 348
: SOFTWARE: FASTSEQ for Windows Version 3.0
:
: SEQ ID NO 339
: LENGTH: 469
: TYPE: PRT
: ORGANISM: Mouse
US-09-188-930-339
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Query Match 60.4%; Score 1499; DB 4; Length 469;  
Best Local Similarity 65.6%; Pred. No. 5.5e-138;  
Matches 274; Conservative 73; Mismatches 71; Indels 0; Gaps 0;

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QY 60 EKKITFTGDNKDKGIDFEFMKYLKDHEKKMLAFKSLDKNNDKGKIEASIVSLQTLG 119
DB 52 KKKIVAGGKDLDDGQDFEEFVHYLDHEKKLLVFKSLDKKNDGRIDAEIMQSLRDLG 111
QY 120 LRTSEQAELILGDSIDVDGTMVDMNEMRDYPLFNPVTDLEELIRPKHSTGIDIGSLT 179
DB 112 VKTSEQAELILGDSIDVDGTMVDMNEMRDYPLFNPVTDLEELIRPKHSTGIDIGSLT 171
QY 180 IPDEFTEDEKSGGOWRROLLAGSIAGAVSRTSTAPDLRLKIMQVHSGSKSDKNINIGGFR 239
DB 172 VPDEFVEBERQGTMMWRHLVAGGAGAVSRTCAPLDLRLKVLQVHASRNNNCIYGGFT 231
QY 240 QMKKEGINSLVMGNGSTNVYKIAPEYAVKFWAYEQTKLLTEBGOKIGTFERRISGSMAG 299
DB 232 OMIREGAGKSLMGNGINVLKIAPEYAVKFWAYEQTKLLTEBGOKIGTFERRISGSMAG 291
QY 300 ATQQTIVPEYVKKTRLAGVKGTOGYSGYDCAKILKHGEGAFYKGYVNNLIGIIPYAG 359
DB 292 ATRQSSITPEYVKKTRLAGVKGTOGYSGYDCAKILKHGEGAFYKGYVNNLIGIIPYAG 351
QY 360 IDLAVYELKSWLDNFANDSVNPGYVLLGCGALSTGQGLASYPDLAVTRFMQAQAML 419
```

Db 352 IDLAVYETLKNLTWLRQYAVNSADPGVFNLLACGTTISSTGOLASYPALVTRMQAASI 411  
OY 420 EGSPOLNMVGLPFRRIISKEGIPGLYRGITPNNFMKVLPAVGISYVYENKOTLGYTOK 477  
DB 412 ECAPEYTHMSLTKQILRTGAGLIRGLAPNFMKVIPIANISISYVENKITLGVQSR 469

RESULT 2  
US-09-188-930-142

; Sequence 142, Application US/09188930A  
; Patent No. 6150502  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murison, James Greg  
; TITLE OF INVENTION: Compositions Isolated From Skin Cells  
; FILE REFERENCE: 11000.1011c1  
; CURRENT APPLICATION NUMBER: US/09/188,930A  
; CURRENT FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 348  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 142  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-188-930-142

Query Match 36.7%; Score 910; DB 4; Length 312;  
Best Local Similarity 63.2%; Pred. No. 1e-80;  
Matches 165; Conservative 51; Mismatches 45; Indels 0; Gaps 0;

OY 60 EKIITGVDYKDGKIDPEEPKYLKQHEKKLAFKSIDKNDGKIEASELYOSLOTIG 119  
DB 52 KQKIYAGKDKLDGDLDEEFVHYLDQHEKKLRLVFKSIDKNDRIQAOEIMOSLRDG 111  
OY 120 LTISSQAEILQSIDVDQVTVDNEMRDYFLFNPVTDIEETIRPKHSTGIDGSLT 179  
DB 112 VAISSQAEKILSKMDKNKTITIDNEMRDYHLHVEWIPILILYKXSTIFDVENLT 171  
OY 180 IPDETEDEKSKGQWROLLAGIAGAVSRSTAPLDRILKIMQVHSGSKDMNIFGGR 239  
DB 172 VDEFTVEEROTGMMWRHLVAGGAGAVSRCTAPLDRILKIMQVHASRNNMCIGFPT 231  
OY 240 QMVRGGGIRSLRNGTINIKIAPETAVYFAYEQYKILTEEGOKIGTFEFGISNAG 299  
DB 232 OMIRGGAGSLMRNGINVLKIAPESAIKEMAYEQMKRLVGSDOETLRHERLVAGSLAG 291  
OY 300 ATAQFTIYPMVAKTRLAGVK 320  
DB 292 AIAQSIYPMVYKTRMALRK 312

## RESULT 3

US-08-961-871-10  
; Sequence 10, Application US/08961871  
; Patent No. 6013858  
; GENERAL INFORMATION:  
; APPLICANT: Wallace, Douglas C.  
; APPLICANT: Graham, Brett H.  
; APPLICANT: Macgregor, Grant R.  
; TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine  
; TITLE OF INVENTION: Nucleotide Translocator Protein and Methods  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Mannattan Circle, Suite 201  
; CITY: Boulder  
; STATE: Colorado  
; COUNTRY: US

; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,871  
FILING DATE: 31-OCT-1997  
CLASSIFICATION: 800

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/030,017  
FILING DATE: 01-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Feiber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 78-96  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089

## INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:  
LENGTH: 298 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-961-871-10

Query Match 14.0%; Score 347; DB 3; Length 298;  
Best Local Similarity 32.2%; Pred. No. 1e-25;  
Matches 95; Conservative 58; Mismatches 114; Indels 28; Gaps 10;

OY 196 ROLLGAGIAGAVSRSTAPLDRILKIMQV-HGSK---SDKM--NIEGPRQVKEGGIRS 249  
DB 10 KPLFAGGIAAASKTRAVAFIERVKILLOYQHSKQISAEKQYKGIIDCVRIKPKQGFIS 69  
OY 250 IMRGNSTVNIKIAPETAVYFAYEQYKILTEEGOKIGTFEFGISGM---AGATAQT 304  
DB 70 FWRGNLANVIRFEPQALNFAFKDKYKQIFLGVDNRHQFWRYFAGNLASGAGATSLC 129  
OY 305 FIYPEHVAKTRLA--VGKTG---QYSGIYDCAKILKHEGLGAFKGYVNNLGIITIPAG 359  
DB 130 EYVPLDFARTTIAADVAGKSSQGRFNGLDCLTKIFKSDGLGLYGFVSVOGIITIPRA 189  
OY 360 IDLAVYELLKSYWLDNFAKDSVNPVWVLLGCGALSTGOLASYPALVTRMQAAML 419  
DB 190 AFEVGYDTRK-----GMLPDPKNVHIIVSMIAOSTVAVAGLVSPFDVRRRRMMQSGR 244  
OY 420 EGSPOL--NMVGLPFRRIISKEGIPGLYRGITPNNFMKVLPAVGISY--VYENMKQ 470  
DB 245 KGADIMYTGTLDCWKRIAKDEGANAFKGAWSN---VLKMGCAVLVLVYDEIKK 296

## RESULT 4

US-09-068-140A-15  
; Sequence 15, Application US/09068140A  
; Patent No. 6281409  
; GENERAL INFORMATION:  
; APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor  
; APPLICANT: and Rex Michael Brennan  
; TITLE OF INVENTION: Blackcurrant Promoters and Genes  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

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Query Match	13.0%;	Score 323.5;	DB 4;	Length 328;
Best Local Similarity	29.7%;	Pred. NO. 2.3e-23;		
Matches	85;	Conservative	53;	Mismatches 131;
			Indels	17;
			Gaps	6;

[illegible]

RESULT 5  
 US-09-068-140A-10  
 : Sequence 10, Application US/09068140A  
 : Patent No. 6281409  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor  
 : APPLICANT: and Rex Michael Brennan  
 : TITLE OF INVENTION: Blackcurrant Promoters and Genes  
 :  
 : NUMBER OF SEQUENCES: 15  
 :  
 : CORRESPONDENCE ADDRESSES:  
 : ADDRESSEE: Smithkline Beecham Corporation  
 : STREET: 709 Swedeland Road  
 : CITY: King of Prussia  
 : STATE: PA  
 : COUNTRY: USA

```

1 ZIP: 19406-0939
2
3 COMPUTER READABLE FORM:
4
5 MEDIUM TYPE: Floppy disk
6
7 COMPUTER: IBM PC compatible
8
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10
11 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
12
13 CURRENT APPLICATION DATA:
14
15 APPLICATION NUMBER: US/09/068,140A
16
17 FILING DATE:
18
19 CLASSIFICATION:
20
21 PRIOR APPLICATION DATA:
22
23 APPLICATION NUMBER: PCT/EP96/04807
24
25 FILING DATE: No. 6281409ember 4, 1996
26
27 ATTORNEY/AGENT INFORMATION:
28
29 NAME: Dinner, Dara L.
30
31 REGISTRATION NUMBER: 33,680
32
33 REFERENCE/DOCKET NUMBER: C70237
34
35 TELECOMMUNICATION INFORMATION:
36
37 TELEPHONE: 610-270-5017
38
39 TELEFAX: 610-270-5090
40
41 TELEX:
42
43 INFORMATION FOR SEQ ID NO: 10:
44
45 SEQUENCE CHARACTERISTICS:
46
47 LENGTH: 289 amino acids
48
49 TYPE: amino acid
50
51 STRANDEDNESS: unknown
52
53 TOPOLOGY: unknown
54
55 MOLECULE TYPE: peptide
56
57 HYPOTHEICAL: YES
58
59 ANTI-SENSE: NO
60
61 FRAGMENT TYPE: N-terminal
62
63 ORIGINAL SOURCE:
64
65 ORGANISM: Ribes nigrum
66
67 STRAIN: Ben Alder
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Query Match	12.6%	Score 311.5	DB 4	Length 289;
Best Local Similarity	29.5%	Pred. No. 2.8e+22;		
Matches	83;	Conservative	51;	Mismatches 130;
				Indels 17;
				Gaps 6;

[illegible]

RESULT 6  
US-08-9337-750C-12  
: Sequence 12, Application US/089337500C  
: Patent No. 593242  
: GENERAL INFORMATION:  
: APPLICANT: Lal, Preeti  
: APPLICANT: Hillman, Jennifer L.  
: APPLICANT: Bandman, Olga  
: APPLICANT: Shah, Purni  
: APPLICANT: Au-Young, Janice  
: APPLICANT: Yue, Henry

```

1  APPLICANT: Guegler, Karl J.
2  APPLICANT: Corley, Neil C.
3  TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
4  NUMBER OF SEQUENCES: 98
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE: Incyte Pharmaceuticals, Inc.
7  STREET: 3174 Porter Drive
8  CITY: Palo Alto
9  STATE: CA
10 COUNTRY: USA
11 ZIP: 94304
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Diskette
14 COMPUTER: IBM Compatible
15 OPERATING SYSTEM: DOS
16 SOFTWARE: FASTSEQ for Windows Version 2.0
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/933.750C
19 FILING DATE: September 23, 1997
20 CLASSIFICATION: 536
21 PRIOR APPLICATION NUMBER:
22 APPLICATION NUMBER:
23 FILING DATE:
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Billings, Lucy J.
26 REGISTRATION NUMBER: 36,749
27 REFERENCE/DOCKET NUMBER: PF-0356 US
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 415-855-0555
30 TELEFAX: 415-845-4166
31 TELEX:
32 INFORMATION FOR SEQ ID NO: 12:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 320 amino acids
35 TYPE: amino acid
36 STRANDEDNESS: single
37 TOPOLOGY: linear
38 IMMEDIATE SOURCE:
39 LIBRARY: SPINNOT02
40 CLONE: 207452
41 JS-08-933-750C-12

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Query Match	11.9%	Score 295	DB 2	Length 320
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			Gaps	10
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D 5 DPKPDGRNNKTEFOYAVNASVSGLYTRALISPDYKIRFOLHEHLSRSDPSAKKHGIIQ	64			
QY 239 --RQWKEGGIRSLWRNGSTVYIKIAPETAWFMYEDQYKLLLEGGKIGTFE-----	290			
D 65 ASROLLOEGEPTAFWKGHVPAQILSIGVAQOLFSE---MLTELVHNGSYDDAREFSV	120			
QY 291 RFISSMAGAIAPQTIITYMEVWKTYLAV-KGTQYSGIYDCAKILKHEGCAFTKGYVP	349			
D 121 HFVCGGLACMACTLVHPVDYLRTFFAAQGEKPYVNTLRHNAVGTMYRSRDPVFYKGLAP	180			
QY 350 NLLGIIPAGIDLAYELLKS-YWLDNPAKDSVNGCVWLLGCGALSSTCGLASVPLAL	408			
D 181 TLIALFPYAGLOFQSCYSSLSKHLKYKALPAEGKKNENLNL-CGSGAGAYISTVLYPDL	239			
QY 409 VRTRQAQAMLEGSPQLMNV---GLF---RRIISKEGIGLGRSITPEFMKVLPAVGS	461			
D 240 EKRRLOVGGFEHARARFQGVRRYKGLMCAKOVLOKEGALGFKKLSPLKAAALSTGPM	299			
QY 462 YVYE 466				
D 300 FFSYE 304				

```

US-09-234-613-12
US-09-234-613, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234.613
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933.750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SPINNOT02
CLONE: 207452
US-09-234-613-12

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[illegible]







Db 251 FV--AGISCTVAATLTPEDVYKTOQOVALGAMEAVRNPLHVDSTWLLRIRAESGT 308  
QY 441 PGLYRGITPNEKMLPAVGISYVYE-----NMKOTLG 473  
Db 309 KGLFAGFLPRIRKRAFPSCAIMISTYFEGKSFFORLNDRLIG 350

RESULT 12  
US-08-775-009-32  
; Sequence 32, Application US/08775009  
; Patent No. 5935783  
; GENERAL INFORMATION:  
; APPLICANT: Gong, Wellong  
; APPLICANT: Emanuel, Beverly S.  
; APPLICANT: Budarf, Marcia L.  
; APPLICANT: Roe, Bruce  
; TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digestion and  
; TITLE OF INVENTION: Veliocardiofacial Syndrome Minimal Critical Region  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Mashburn Kurtz Mackiewicz &  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/775,009  
; FILING DATE: 27-Dec-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trujillo, Doreen Yanko  
; REGISTRATION NUMBER: 35,719  
; REFERENCE/DOCKET NUMBER: CH-0681  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 311 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-775-009-32

Query Match 9.7%; Score 239.5; DB 2; Length 311;  
Best Local Similarity 25.4%; Pred. No. 3.5e-15;  
Matches 74; Conservative 58; Mismatches 142; Indels 17; Gaps 7;  
QY 196 ROLLAGGAGVSRSTAPDRKIMQV-HGSKSDKMNIFGG-FRQMEGGIRSRMRG 253  
Db 27 KALLAGLGGAGTICTFPEYVKTQQLDERSHPRRYRGIGCVRTVSHGLGLYRG 86  
QY 254 NGTNVIRIKAPETAVFMAVEQYKLLTEEGOKIGTFEERFISGSMAG-ATQTFIYMEVM 312  
Db 87 LSLVLGSIKPAVRFQMEFELSNHMRDAGRIDSTRGLGLGAGVAELAVVVCPRMETV 146  
QY 313 KTLAVAGKIG--QYSGIYDCAKILKHESLGAIFYGYPNLLGIIPYAGIDLAAYVELK 369  
Db 147 KYVFIHQDQSPNPKYRGFFHGVREIYEDGLKGTQGLTATVTKOGSNOAIRFFVMTSLR 206  
QY 370 SYVLNDPRAKSVNP--GVAVLLGCGALSTGQGLASYPALVTRTRMOAAMLEGSQNL 426  
Db 207 NMYRGDNPKNRPMPLITGV-----GAIAGASVFGNTPLDVIKTRMQG--LEAHKYNR 258

QY 427 MGLFRRIISKEGIPGLYRGITPNEKMLPAVGISYVYENMKOTLGTVOK 477  
Db 259 TWDGGLQILKKKEGLKAFYKGFPRIGRCVDAIVFYIDVYKLLNKVMK 309

RESULT 13  
US-08-518-878B-56  
; Sequence 56, Application US/08518878B  
; Patent No. 5702902  
; GENERAL INFORMATION:  
; APPLICANT: Tartaglia, Louis A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/518,878B  
; FILING DATE: 23-Aug-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cornuzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-036  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/88864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 299 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; US-08-518-878B-56

Query Match 9.4%; Score 233.5; DB 1; Length 299;  
Best Local Similarity 25.3%; Pred. No. 1.3e-14;  
Matches 75; Conservative 50; Mismatches 138; Indels 33; Gaps 9;  
QY 197 QLLAGTAGAVSRSTAPDRKIMQVHGSKSDKMNIFGGFRQMEGGIRSRMRG 247  
Db 6 KFLGAGTAACIADITPELPDRKVRLOIGESQSPVATVSAQYRGWGTILITVWREGP 65  
QY 248 RSLMRGNGTNTKAPFAVFMAYEYKLLTEEGOKIGTFEERFISGSMAGATAQFRIY 307  
Db 66 RSLVINGLVAGIORMSASVIRIGLYDSYKQFTYTGSEHASTGSLLAGSTGALAVAAQ 125  
QY 308 PMEVMKTRL-AVCKTG--QYSGIYDCAKILKHESLGAIFYGYPNLL-GIIPYAGID 361  
Db 126 PTDVVKVRFQAOAAGAGGRYQSTVNAYKTILAREGFGMLKGTSPNVARAIVNCA--E 183  
QY 362 LAYVELLKSYWLD-NFKKDSVNPQVWVLLGCGALSTGQGLASYPALVTRTRMOAAMLE 420  
Db 184 LVTYDILKDLKLNMTDDELPCHTSAFAG--ECTYVIAAPVQVVKTRVNNKSLGQ 239  
QY 421 ----GSPQLMNVGAFRRRIISKEGIPGLYRGITPNEKMLPAVGISYVYENMKOTL 472  
Db 240 YSSAGHCAIIM-----LQKESPRATYKGFMPFRLGSGNNVVMFVYTEDLKAAL 288

RESULT 14

US-08-470-868A-56  
; Sequence 56, Application US/08470868A  
; Patent No. 5861485  
; GENERAL INFORMATION:  
; APPLICANT: Tartaglia, Louis C.  
; TITLE OF INVENTION: Compositions and Methods for the  
; TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie and Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/470,868A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-0031-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66441 PENNIE  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 299 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; US-08-470-868A-56

Query Match 9.4%; Score 233.5; DB 2; Length 299;  
Best Local Similarity 25.3%; Pred. No. 1.3e-14;  
Matches 75; Conservative 50; Mismatches 138; Indels 33; Gaps 9;  
QY 197 OLLAGGAGVARTSPAPDRLLKIMOVHGSKSDKM-----NIFGFRQMYKEGI 247  
DB 6 KFLGAGTACACIDLTFFPLDTAKVRLQIOGESQGPYRATVSQYKGVMTILLTWRTGEP 65  
QY 248 RSLMNGNGTNVIAIPETAIVKFMAYEQYKLLJTEGQKIGTFEERFISGMAGATAQTFY 307  
DB 66 RSLYNGLVAGLQROMSFASVRIGLYDSVQKQFYTKGSEHASICSRLLAGSTGALAVANQ 125  
QY 308 PHEVAKTRL-ANGKTG---QYSGIYDCAKKILKHEGLAFYGYVNNL--GIIPYAGID 361  
DB 136 PPDVYKVRQQAQARAGGRRYSTVNAKYTTIAREGFRGLMKGTSBNARNAIVNCA--E 183  
QY 362 LAVVELLSKYWD-NFAKDSVNPBGVWVLLCGALSTGCGLASYPPLAVRTBMQAAMLE 420  
DB 184 LVTYDLIKALKANIMTDDLPCHFTSAFAG-----FCTTVIASPYDVYKTYRMSALGO 239  
QY 421 ---GSPOLNMGVLFRRRIISKEGIPGLYRGITPNFMKYLPAVGISVYVENKQTL 472  
DB 240 YSSAGHCALTM-----LQKGPRAFYKGFMPSPFLRLGSMVWVMEVYEQKRAL 288

RESULT 15  
US-08-518-878B-51  
; Sequence 51, Application us/08518878B  
; Patent No. 5702902  
; GENERAL INFORMATION:  
; APPLICANT: Tartaglia, Louis A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

; TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/518,878B  
; FILING DATE: 23-AUG-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-036  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 309 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; US-08-518-878B-51

Query Match 9.4%; Score 233.5; DB 1; Length 309;  
Best Local Similarity 25.3%; Pred. No. 1.3e-14;  
Matches 75; Conservative 50; Mismatches 138; Indels 33; Gaps 9;  
QY 197 OLLAGGAGVARTSPAPDRLLKIMOVHGSKSDKM-----NIFGFRQMYKEGI 247  
DB 16 KFLGAGTACACIDLTFFPLDTAKVRLQIOGESQGPYRATVSQYKGVMTILLTWRTGEP 75  
QY 248 RSLMNGNGTNVIAIPETAIVKFMAYEQYKLLJTEGQKIGTFEERFISGMAGATAQTFY 307  
DB 76 RSLYNGLVAGLQROMSFASVRIGLYDSVQKQFYTKGSEHASICSRLLAGSTGALAVANQ 135  
QY 308 PHEVAKTRL-ANGKTG---QYSGIYDCAKKILKHEGLAFYGYVNNL--GIIPYAGID 361  
DB 136 PPDVYKVRQQAQARAGGRRYSTVNAKYTTIAREGFRGLMKGTSBNARNAIVNCA--E 193  
QY 362 LAVVELLSKYWD-NFAKDSVNPBGVWVLLCGALSTGCGLASYPPLAVRTBMQAAMLE 420  
DB 194 LVTYDLIKALKANIMTDDLPCHFTSAFAG-----FCTTVIASPYDVYKTYRMSALGO 249  
QY 421 ---GSPOLNMGVLFRRRIISKEGIPGLYRGITPNFMKYLPAVGISVYVENKQTL 472  
DB 250 YSSAGHCALTM-----LQKGPRAFYKGFMPSPFLRLGSMVWVMEVYEQKRAL 298

Search completed: August 18, 2002, 09:20:56  
Job time: 4010 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2002, 08:23:51 ; Search time 43.26 Seconds  
(without alignments)  
1059.515 Million cell updates/sec

Title: US-09-777-921A-2  
Perfect score: 2481  
Sequence: 1 MLRWLRDLPALPTAACODAEQ.....VGISVYVENKQTIGVTQK 477

Scoring table: BLASTSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2373	95.6	475	2	T50686 peroxisomal Ca-dep
2	1103	44.5	588	2	T22688 hypothetical prote
3	991.5	40.0	531	2	G89667 protein FIVE.2 (1
4	988.5	39.8	587	2	T21074 hypothetical prote
5	852	34.3	479	2	T49871 peroxisomal Ca-dep
6	521	21.0	352	2	T01729 mitochondrial solu
7	520	21.0	332	2	T47703 Ca-dependent solu
8	506	20.4	358	2	T45934 hypothetical prote
9	500.5	20.2	500	2	T39385 probable mitochon
10	480.5	19.4	330	2	S26596 Graves disease mit
11	475	19.1	348	2	D84798 probable mitochon
12	455.5	18.4	415	2	T48171 hypothetical prote
13	454.5	18.3	381	2	T51158 hypothetical prote
14	448	18.1	325	2	T04273 hypothetical prote
15	446	18.0	392	2	T05350 adenylate transloc
16	430.5	17.4	349	2	A40141 mitochondrial solu
17	429.5	17.3	294	2	T22145 hypothetical prote
18	428	17.3	326	2	B40141 mitochondrial solu
19	425.5	17.2	418	2	B96811 hypothetical prote
20	425.5	17.2	436	2	T01459 B1 protein precur
21	417.5	16.8	326	2	S57544 probable membrane
22	392	15.8	326	2	T37874 probable membrane
23	377.5	15.2	494	2	S57539 probable membrane
24	369	14.9	298	2	B43646 ADP,ATP carrier pr
25	368	14.8	298	1	S03894 ADP,ATP carrier pr
26	365	14.7	357	2	S46795 ADP,ATP carrier pr
27	356	14.3	301	2	S51132 ADP,ATP carrier pr
28	355.5	14.3	386	2	S21974 ADP,ATP carrier pr
29	355.5	14.3	387	2	S14876 ADP,ATP carrier pr

30	355	14.3	298	2	I60173 adenine nucleotide
31	354.5	14.3	387	2	S16568 ADP,ATP carrier pr
32	354	14.3	305	2	S68154 ADP,ATP carrier pr
33	353.5	14.2	309	2	A24849 ADP,ATP carrier pr
34	353	14.2	298	2	S37210 ADP,ATP carrier pr
35	352.5	14.2	366	2	S17917 ADP,ATP carrier pr
36	352	14.2	298	1	A44778 ADP,ATP carrier pr
37	352	14.2	339	2	A41677 ADP,ATP carrier pr
38	351.5	14.2	318	1	A31978 ADP,ATP carrier pr
39	351	14.1	298	1	A29132 ADP,ATP carrier pr
40	349.5	14.1	382	2	S33630 ADP,ATP carrier pr
41	349.5	14.1	386	2	T09709 ADP,ATP carrier pr
42	348	14.0	298	1	XWBO ADP,ATP carrier pr
43	347	14.0	298	2	S31814 ADP,ATP carrier pr
44	346	13.9	385	1	S29852 ADP,ATP carrier pr
45	345	13.9	313	1	XWNC ADP,ATP carrier pr

ALIGNMENTS

Query Match	95.6%	Score 2373;	DB 2;	Length 475;
Best Local Similarity	95.2%	Pred. No. 4.8e-149;		
Matches 454;	Conservative 12;	Mismatches 9;	Indels 2;	Gaps 1;
QY 1 MLRWLRDLPALPTAACODAEPTRETLFOALDRMGDVVDIGLEGLRNGTIPLGDAE 60				
DB 1 MLRWLRDLPALPTAACODAEPTRETLFOALDRMGDVVDIRELEGLSLGIPLGDAE 60				
QY 61 EKIFTTGVDVKKDKLDPEEFPMKYLKDHEKKMLAFKSLDKNNDKIRASEIVOSLOTIGL 120				
DB 61 EKIFTTGVDVKKDKLDPEEFPMKYLKDHEKKMLAFKSLDKNNDKIRASEIVOSLOTIGL 120				
QY 121 TISEQDAELILQSIDVDGVTVDWNEWRDYFLNPVTDIEIIRFMKHSIGIDISLTI 180				
DB 121 TISEQDAELILQSIDVDGVTVDWNEWRDYFLNPVADIEIIRFMKHSIGIDISLTI 180				
QY 181 PDPEFTEDEKSSGGQWQOLLAGTAGAASRSTAPLDLKTIMQVHGSKSKMNTGFGRQ 240				
DB 181 PDPEFTEDEKSSGGQWQOLLAGTAGAASRSTAPLDLKTIMQVHGSKSKMNTGFGRQ 240				
QY 181 PDPEFTEDEKSSGGQWQOLLAGTAGAASRSTAPLDLKTIMQVHGSKSKMNTGFGRQ 240				
DB 181 PDPEFTEDEKSSGGQWQOLLAGTAGAASRSTAPLDLKTIMQVHGSKSKMNTGFGRQ 240				
QY 241 MVEEGGIRSLMRNGTINVIKIAETAVKFWAYQYKLLTEESOKITGFRTISGSWAGA 300				
DB 239 MIKEGGSRLMRNGTINVIKIAETAVKFWAYQYKLLTEESOKITGFRTISGSWAGA 300				
QY 301 TAOTFIYPMVKTRILAVGKTGOYSGIYDCAKKILKHESGAFYKGVPMULGIIPYAGI 360				
DB 299 TAOTFIYPMVKTRILAVGKTGOYSGIYDCAKKILKHESGAFYKGVPMULGIIPYAGI 360				
QY 361 DLAVVELKSYWLDNFAKQSVNPGVWVLGGGSLSSCGOLASYPALAVYTRMOAQMLE 420				
DB 359 DLAVVELKSYWLDNFAKQSVNPGVWVLGGGSLSSCGOLASYPALAVYTRMOAQMLE 420				
QY 421 GSPOLMVGLEFRRIISKEGIPGLYRGITTFPMKVLPAVGISYVYVENMKOTLGVTK 477				
DB 421 GSPOLMVGLEFRRIISKEGIPGLYRGITTFPMKVLPAVGISYVYVENMKOTLGVTK 477				

Db 419 GAPQNMVGLFRRIRISKESGLPGIYKRITTFENMKVLEPAVGISYVVEYEMKQTLCVYTK 475

RESULT 2

T22688

hypothetical protein F55A11.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T22688

R:Kershaw, J.

submitted to the EMBL Data Library, May 1996

A:Reference number: Z19600

A:Accession: T22688

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-588 <WIL>

A:Cross-references: EMBL:Z72511; PIDN:CAA96658.1; GSPDB:GN00023; CESP:F55A11.4

A:Experimental source: clone F55A11

C:Genetics:

A:Gene: CESP:F55A11.4

A:Map position: 5

A:Introns: 24/1; 77/2; 277/3; 434/3; 474/1; 511/3; 531/3

Query Match	44.5%	Score 1103	DB 2	Length 588
Best Local Similarly	45.7%	Pred. No. 3.9e-65		
Matches 210	Conservative 104	Mismatches 142	Indels 4	Gaps 3

OY	19	EOPRREYELFALORNGGVYDIELDEGRJNGJLPIPGOAAEKEFTTGVNKGKDFE	78
Db	73	EKERQIRDIYRDLIDNDGTIDIDIDLTLALKHEPHIPLANLAAYIMSKMSPDEGRVDF	132
OY	79	EPMYLYKDHKKMLAFKSLDKNDNGKIEASEIYOSLQTLGLTISEQOABELLOSIDVDB	138
Db	133	SESSVYIENEOKLEAMEADMRNDHNDGVADVDEMKNYCKDGVPLDHKACHIKYNNKDGTG	192
OY	139	TMYDWMNMRPYFLFENYVTDLEELIIRMKHSTGIDIGDSLITIDDEFEDKKSGQMMROL	198
Db	193	SASVDLKEEFOEPMLIYPSDSLKDITVDWRNHLITIDIGEDSOIDPDDTSQOQMORGIMWRHL	252
OY	199	LAGGIAGAVSRSTAPDLRLIKIMYGVGSKDKNMINGGFROWMKIEGJLSLRKNGNTYN	258
Db	253	VAGGAAGAVSTCTAPDRIIVYVLQVWSSKTNRLRGVMSCLLHAEBGJKISPMRNGINYN	312
OY	259	IKIAPETAVKRWAYEYQYKLLTEE--GQKIGTEERITSGSMAGATAQFTIYPEVMAKTRL	316
Db	313	IKIPEBIAIKFMCYDOJLRLQKKGEHELISTEERLCAGSAAASISOSTIYPEMVYKTRL	372
OY	317	AVGTGQGS--GIYDOCAKKILKHEELGAFYGVYVYENLGIIPYAGIDLAVALYELLKSWLON	375
Db	373	ALRRTGQDLRGIITHFAHKMYTKESIRCFYKGYLPLNLGIIIPYAGIDLAIETLKRYYVR	432
OY	376	FAKDSVGVNVALLGGCALSSTGQSLASYPALAYRTMQAOAMLEGSPOLN--MYGLFRRI	434
Db	433	YETNSSBEGVALLACGSCSTGQLSYSPALAYRTLOALSTIRYSPQDVTMGQFKYI	492
OY	435	ISKBEJIGLIGITPNPMKULPANGISIVYVYENMKOTLGV	474
Db	493	LONEGVTVFYRGITIPNFKLYIPAVISYVYVYEEKRTRLG	532

RESULT 3  
C89667 protein F17E5.2 [imported] - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Nov-2001  
C:Accession: C89667  
R:anonymous, The C. elegans Sequencing Consortium.  
A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biological processes.  
A:Reference number: A75000; MUID:99065613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2104, 1999.

A:Accession: G89667  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-331 <STD>  
A:Cross-references: GB:chr\_X; PIDN:CAA90761.1; PID:q3676012; GSPDB:GN00028; CESP:F17E  
C:Genetics:  
A:Gene: F17E5.2  
A:Map position: X  
A:Map position: X

Query Match	40.0%;	Score	991.5;	DB 2,	Length	531;	
Best Local Similarity	42.3%;	Pred. No.	7.7e-58;				
Matches 203; Conservative	92;	Mismatches	138;	Indels	47;	Gaps	8;

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0y 16 ODAEPTVEYETLLFALBRNNGVVDIELOEGJENLIEIPRIGDAEKEEIPFTTGVDNKGK 75
0y 11 QNISLSTIRMYRBLDANDNGSIDIDRLQAL-SIQAHIPASVAPRLBERKSEHSDBY 69
Db 76 DFEEMFKLKDHEKMKMLAFKSLDKNDKGIEASEIYOSIQTGLTISEQOAEILLQSID 135
Db 70 TYADEPTNYVIAHEARLAEVEFKPIDLNSDEGDYAEIKSYCKEMGVMLDDQKMSIYKKMD 129
0y 136 VDGJTVUMNMBRYELFENPYTDEIEELIRPKHSTG-----IDIGDSL 178
Db 130 QSGSSSVMLNEFOPMLYPSBTDNRDWDPMRHNHLYCTCESNSRFRTONFOIIDIEDG 189
0y 179 TIPDEFTDEKSSQWMKQLLJAGAVSSTAPLDRKI-----M 221
Db 190 QVPDEFTQJELLSCGVMRHNHLYAGVACAMSTCAPEDRIKYVLLQWVYLLHLEPHMELKA 249
0y 222 MOVHGSKSDKNINFGFEROMVBECSISLMBNGSTNYIKIAPETAYKFNAYEOKYLLTE 281
Db 250 LQVNSTKTKNGGVAVSCVHLIABEGISFPMGNINVIKIIAPESAMFKCYDIKRMWGE 309
0y 282 --EGOKITFERFRTSGMAGATQTFIYPMENVMTKTRIAVCKQY--SGIYDCAKTKLKEH 338
Db 310 YKGGAELESTERLLAGSSAGAIISOTAIYPMENVMTKTRIALKRTQGLDKGMFHPHKMYTKE 369
0y 339 GLGAFYKGVENLGLIIPYAGIDIAVYELKSYWLDNFPARDSVNPGVYMLLGGALSTFC 398
Db 370 GIKCFYKGYLNLNLGIIPYAGIDITLVYESLKSMY--TKYTEHNEHPGVALLIACGTSSFC 428
0y 399 GOLASYPLALVTRNOQAMLEGGPOLN-----WGLFRKLISKEGIPGLYRBITNPNFK 453
Db 429 GOLASYPLALVTRNOQAAAI--SPKNSSTOPDVTWGGFKHILDEGTGTGRITTPNFK 485

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RESULT 4  
T21074  
hypothetical protein F17E5.2 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-oct-1999 #text\_change 18-Feb-2000  
C:Accession: T21074  
R:McMurray, A.  
submitted to the EMBL Data Library, August 1995  
A:Reference number: Z19368

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-587 <WIL>  
A:Cross-references: EMBL:Z50873; PIDN:CAA90761.2; GSPDB:GN00028; CESP:F17E5.2  
A:Experimental source: clone F17E5  
C:Genetics:  
A:Gene: CESP:F17E5.2  
A:Map position: X  
A:Introns: 21/; 48/3; 74/2; 111/3; 183/2; 384/1; 432/3; 503/1; 541/3

Query Match	39.8%	Score 988.5;	DB 2;	Length 587;
Best Local Similarity	42.3%;	Pred. No. 1.4e-57;		
Matches 202;	Conservative 91;	Mismatches 137;	Indels 47;	Gaps 8.



```

Db 70 EKEKKIDMDYRDLADDDGSDIDRDLQAL-SLQAHIPASVAPKLTLRMKSEHSRDVYA 128
Qy 79 EPKMYLKDHKKKKLAFKSLDKNNDDKILEASEIYQSLQTLGTLTISBQOAILLQSTIDVG 138
Db 129 DFNVIYAHARLARLAEYFDKIDLNSDGEVDAEIKSYCKEKGWNLDDQKAMSIYKMQSG 188
Qy 139 TMTVDNMENRDFLEFNVPTDIEETIRFMKSTG-----IDIDSLTIP 181
Db 189 SSSVNLNEFPDDMLLYSTDMKRDVDFWRNLNVTCLSENSRFRTOQNFQIIDIGEDQVP 248
Qy 182 DEFTEDKSKGQWRRQLLAGIAGVSRSTAPLDRLKI-----MMOY 224
Db 249 EDTPPELLSGVMMRHVLVAGVAGAMSRCTAPDRIRKYLQVWYHLHLRHFIMFLKALQV 308
Qy 225 HGSKSDKMNIFGFGROWKRGGIRSLMRGNTVYIKIAPETAKFMAIEQYKILLTE--E 282
Db 309 NSTRTNKLGVASCVHLHLHAEGGIKSFWRGNGINVIKIAPESAMKFMICYDQIKRMQYK 368
Qy 283 GORIGTFEFTSGSMAGATQFTIYPMVEMKTRILAVGKTGOY-SGIYDCAKKILKHEGLG 341
Db 369 GALESTIERLRLASSAGAIQTAIYPMVEMKTRILALRRTQDLKGMHFHAKMTTKGCIK 428
Qy 342 AAYKGYVNLGIIPYAGIDLAVYELKSYWLDNFADSVNPGVWLLGGALSTGOL 401
Db 429 CFYKGYLPNLGIIPYAGIDLTVEYSLSKMY-TRKYTEHTEPGVLLALACGCSSTGOL 487
Qy 402 ASYPLALVTRMOAMLEBSPOLN-----MVGIFRRIIEKEGIPGLYKRGITPRMK 453
Db 488 ASYPLALVTRLOARAI---SPKNSTOPDMVQGFKHILQTEGPTGLRITPRMK 541

```

## RESULT 5

```

T49871
peroxisomal Ca-dependent solute carrier-like protein - Arabidopsis thaliana
N:Alternate names: protein T211.30
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
C:Accession: T49871
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Le
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24493
A:Accession: T49871
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <BEV>
A:Cross-references: EMBL:AL163912; GSPDB:G000063; ATSP:T211.30
A:Experimental source: cultivar Columbia; BAC clone T211
C:Genetics:
A:Gene: ATSP:T211.30
A:Map position: 5
A:Introns: 133/1; 391/1; 421/2
C:Keywords: peroxisome

```

Query Match 34.3%; Score 852; DB 2; Length 479;

Best Local Similarity 39.4%; Pred. No. 1, le-48;

Matches 181; Conservative 90; Mismatches 172; Indels 16; Gaps 6;

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Qy 19 EDPTRRETFQALDRNGDVGVDIGELQEGRLNIGPLGDAEKEITFTTGDNVKGKLDPE 78
Db 33 ERRIIRSLFDEFDNNLNFLDYDAQIEKGLASIQIPEPKYARDLFRVCANRGRDYQ 92
Qy 79 EPKMYLKDHKKKKLAFKSLDKNNDDKILEASEIYQSLQTLGTLTISBQOAILLQSTIDVG 138
Db 93 EFRRIYDAKELELIRFQALIDVBNHNCILPEELWEALVKAIGITDDEELARFVEHVDKN 152
Qy 139 TMTVDNMENRDFLEFNP-VTDIEEIRFKHSTGIDIGSLTIPDEFTEDKSKGQWRRQ 197
Db 153 NGITFEEMRDFLLVPRHEATLENIYHMERVCLIDIGBAVLPDGIKIVKRS-----RL 208
Qy 198 LLAGIAGAVSRSTAPLDRLKIMMOVHGSKDKNNIFGFGROWKRGGIRSLMRGNTN 257

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```

Db 209 LLAGIAGAVSRSTAPLDRLKVVLYQVRAHA---GVLPITKKIMREDKLMGFFRGNCN 265
Qy 258 VIKIAPETAVKFAVEQYKILLTEEGOKIGTFEERFISSMAGATQFTIYPMVEMKTRL- 316
Db 266 VMKAPESAIKFCAYEMLKPMIIGEDGDIQTSGRIMAGMAGALAQTAIYPMDLVTRLO 325
Qy 317 -AVGKTQYSGIYDCAKILKHEGLGAFYKGYVNLGIIPYAGIDLAVYELKSYWLDN 375
Db 326 TCVEGKAPKRLMLKTRLDIWRRECPRAFYKGLFPSLIGITVYAGIDLAAYETLQDLSRTY 385
Qy 376 FAKDSVNPQWVLLGGALSTGQOLASYPALVTRMOAMLEBSPOLNMGIFRRII 435
Db 386 ILQOT-BPGPLIQSCGWTSGALGASCVPLQVVRTRMOAD-----SKTKMQKEFNMTM 439
Qy 436 SKGIPGLYKRGITPRMKVLPVAGISYVYENMQTLGV 474
Db 440 KGEGLRGEYRGLPLNLKVPAAISITYIYEMAKKNMAL 478

```

## RESULT 6

T01729

mitochondrial solute carrier protein homolog - Arabidopsis thaliana

N:Alternate names: protein A.IG002N01.16

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 24-Nov-1999

R:Scheet, P.; Magg, L.

submitted to the EMBL Data Library, June 1997

A:Description: The sequence of A. thaliana IG002N01.

A:Reference number: Z14407

A:Accession: T01729

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1352 <SCH>

A:Cross-references: EMBL:AF007269; NID:g2191126; PID:g2191150

A:Experimental source: cultivar Columbia

C:Genetics:

A:Map position: 4

A:Introns: 51/2; 67/3; 122/2; 135/1; 172/3; 210/3; 325/3

A:Note: A.IG002N01.16

C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology

C:Keywords: mitochondrion

Query Match 21.0%; Score 521; DB 2; Length 352;

Best Local Similarity 36.7%; Pred. No. 4, 9e-27;

Matches 115; Conservative 64; Mismatches 94; Indels 40; Gaps 9;

```

Qy 196 ROLLAGIAGAVSRSTAPLDRLKIMMOVHGSKDKNN-IFGFGROWKRGGIRSLMRGN 254
Db 40 KSLFAGGVAGGVSRKTAVAPLERKILQVONPHRIKISGYOGIKHIMRTGELGTRGN 99
Qy 255 GTNVYIKIAPETAVKFAVEQ-----YKLLTEGOKIGTFEERFISSMAGATQFTI 306
Db 100 GTNCARIVPNSAVKFFSEYEQASNGILYMYRQRTGENAQLPLRLRLGAGATAGIAMSAT 159
Qy 307 YPMVEMKTRILAVKGTG---QYSGIYDCAKILKHEGLGAFYKGYVNLGIIPYAGIDLA 363
Db 160 YPMVEMKTRILAVKGTG---QYSGIYDCAKILKHEGLGAFYKGYVNLGIIPYAGIDLA 363
Qy 364 VYELKSYWLDNFADKDSVNP-----GVWLLGGALSTGQOLASYPALVTRMO 414
Db 220 VYELSLD-WL---VKE--NRYGLVENNELTVYRLTGALAGYQGIATPFLDYIRRMQ 273
Qy 415 -----AQAMLEBSPQ-----LNNVGLFRRIISKEGIPGLYKRGITPRMKVLPVAGIS 461
Db 274 MVGMDASAIYVTEGSRSTASLEYTGWADARFKTVRHGFGALYKGLVPSNVKVPSTATA 333
Qy 462 YVYVEMKQTLGV 474
Db 334 FVYVEMKQTLGV 346

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Db 327 DPQDVKLPGNLVMAFGALSGSTGATVFPDLNLTIRLQTOGSHAPATYDG-----FIDC 381  
 QY 431 FRRISKEGIPGLYRGITPFPKMLVPAGISVYVENMKOTGV 474  
 Db 382 FFKTTTNEGFRGLYKGLSPNLKLVAPSAISTYLVENCKKMLGL 425

# RESULT 10

526596

Graves disease mitochondrial solute carrier protein - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 05-Nov-1999  
 C:Accession: S26596; 146022

R.Flemonste, G.; Runswick, M.J.; Walker, J.E.; Palmerl, F.  
 submitted to the EMBL Data Library, May 1992

A:Description: Sequence and pattern of expression of a bovine homologue of a human mitoc  
 A:Reference number: S26596  
 A:Accession: S26596  
 A:Status: preliminary  
 A:Molecule type: mRNA

A:Residues: 1-330 <FID>  
 A:Cross-references: EMBL:X66035; NID:g386; PIDN:CAA46834.1; PID:g387  
 R.Flemonste, G.; Runswick, M.J.; Walker, J.E.; Palmerl, F.  
 DNA Seq. 3, 71-78, 1992

A:Title: Sequence and pattern of expression of a bovine homologue of a human mitochontri  
 A:Reference number: 146022; MUID:93091248  
 A:Accession: 146022

A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-330 <FID>

A:Cross-references: EMBL:X66035; NID:g386; PIDN:CAA46834.1; PID:g387  
 C:Genetics:  
 A:Gene: GDC

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
 C:Keywords: cardiac muscle; duplication; heart; mitochondrion; transmembrane protein  
 F:31-119/Domain: ADP, ATP carrier protein repeat homology <ACPI>  
 F:125-215/Domain: ADP, ATP carrier protein repeat homology <ACP2>  
 F:235-327/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 19.4%; Score 480.5; DB 2; Length 330;  
 Best Local Similarity 38.1%; Pred. No. 2.1e-24;  
 Matches 112; Conservative 54; Mismatches 109; Indels 19; Gaps 8;

QY 194 WROLLAGTAVSRSTAPLRLKIMQVHSGSKDNINFGPROMKEGIRSLMRG 253  
 Db 34 WLRSTLAGGACCAKTTAPLDRVAVLQAHNHHTRHVGSTLRAVKKBEYGLGKYG 93  
 QY 254 NCTNVKIAPEYAVKFAVEYOYKLLTERGOKIGTFEPISSMGAGATQTFIYPMEMVK 313  
 Db 94 NCAMMIRIPYGAIOFMAFEHKTLLTKLGSGVHVRMLMAGSMGCMTAVICTYPLDMVR 153  
 QY 314 TRLAVKGTQ--YSGIYDCAKKILKHEG--LCAFTKGIYPNLGIIPVAGIDLAVELK 369  
 Db 154 VRLAFOVKGHEHTYTGTHAFKTIYAKEGGFLG-FYRGMLPTILGMAPYAGVSFFETGLK 212  
 QY 370 SYWLNEFA-----KDSVYGVWVL-----LGGALSSFCGGLASPLALVTRMAQAM 418  
 Db 213 SYGL-SYAPTLIGRPSSDNPVNLVTKTHNLGCGVAGAIADTISTPDPVTRRRMOLGAV 271  
 QY 419 L-EGSPOLNMGVLFRRISKEGI-DGLYRGITPFPKMLVPAGISVYVENMKO 470  
 Db 272 LPEFKCLTMRFTMKYVYGHGIRGLYGLSLNLYRCVPSQAVAFYTELKMO 325

# RESULT 11

DB4798

probable mitochondrial carrier protein [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001

C:Accession: DB4798  
 R.Li, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

uess, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter  
 Nature 402, 761-768, 1999  
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: A84420; MUID:20083487

A:Accession: DB4798  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-348 <STO>

A:Cross-references: GB:AE002093; NID:g4895195; PIDN:AAD32782.1; GSPDB:GN00139  
 C:Genetics:  
 A:Gene: At2g37890

A:Map position: 2  
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
 C:Keywords: mitochondrion

Query Match 19.1%; Score 475; DB 2; Length 348;  
 Best Local Similarity 36.7%; Pred. No. 5.2e-24;  
 Matches 114; Conservative 52; Mismatches 103; Indels 42; Gaps 9;

QY 195 WROLLAGTAVSRSTAPLRLKIMQVHSGSKD-----KNINIGFQPMKEGIR 249  
 Db 42 FQNLGAGTGAISKTCTAPLRLTLFQLQMGQSEGAVLSRNLREASRIINEGYRA 101  
 QY 250 LMRNGNTVNIKIPETAVKFAVEYOYKLLTER-----GOKIGT-FEPISSMGAGAT 301  
 Db 102 FMKGNLVTVYHRIPTAVNFAVEYKTNLFNPNVQSFIGNTSGNPVIFVFGGLAGIT 161  
 QY 302 AQTFIYPMEMVKTRAVKGTG--OYSGIYDCAKKILKHEGIAFYKGVYPNLGIIPYAGI 360  
 Db 162 AATATVPLDLVTRRLAQRNAIYVGGIEHTEFRICREGLIGLYKGLAVLLGVPGLAI 221  
 QY 361 DLAVYFELKSYWIDNFAKDS-----VNRGVWVLGGALSSFCGGL-----ASTPLA 407  
 Db 222 NEFAVSMKLEFMWSHHPNDLVLSVSGGL-----AGAVSSTDGKLFDAHNVATYPLD 276  
 QY 408 LVYTRMAQAMLEGSP-----OLNMVGLFRRISKEGIPGLYRGITPFPKMLVPAGIS 461  
 Db 277 LVRRMO-----VEGAGGARVYNTGLEGFTPKHLFKSGFGITRGILPEYKKVYPGVGIY 332  
 QY 462 YVYVENMKOTL 472  
 Db 333 FMYDALRLLL 343

# RESULT 12

T48171

hypothetical protein F7A7.20 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000

C:Accession: T48171  
 R.Bevan, M.; Terryn, N.; Ardiles, W.; Buyschaert, C.; Dasseville, R.; De Clerck, R.;  
 ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.  
 submitted to the Protein Sequence Database, March 2000

A:Reference number: 224487  
 A:Accession: T48171  
 A:Status: preliminary  
 A:Molecule type: DNA

A:Residues: 1-415 <BEV>  
 A:Cross-references: EMBL:AL161946

A:Experimental source: cultivar Columbia; BAC clone F7A7  
 C:Genetics:  
 A:Map position: 5

A:introns: 144/3; 163/3; 184/3; 203/3; 231/3; 254/3; 292/2; 349/1; 375/2  
 A:Note: F7A7.20

Query Match 18.4%; Score 455.5; DB 2; Length 415;  
 Best Local Similarity 33.1%; Pred. No. 1.3e-22;  
 Matches 107; Conservative 66; Mismatches 115; Indels 35; Gaps 8;

QY 177 SLTIPEFTDEKKSQWMO-----DLAGGAGAVSRSTAPLDRKIM 222  
 Db 177 SLTIPEFTDEKKSQWMO-----DLAGGAGAVSRSTAPLDRKIM 222





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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2002, 09:23:05 ; Search time 24.8 Seconds  
(without alignments)  
744,727 Million cell updates/sec

Title: US-09-777-921A-2  
Perfect score: 2481  
Sequence: 1 MLRWLRDFALEPTACODAEQ.....VGISVYVENMKQTIGVTOK 477

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1103	44.5	588 1	CMC2_CAEEL
2	988.5	39.8	587 1	CMC3_CAEEL
3	611.5	24.6	545 1	CMC1_YEAST
4	480.5	19.4	330 1	GDC_BOVIN
5	454.5	18.3	332 1	GDC_HUMAN
6	428	17.3	322 1	GDC_RAT
7	425.5	17.2	436 1	BRL_MAIZE
8	392	15.8	326 1	YE08_SCHPO
9	369	14.9	298 1	ADT3_BOVIN
10	368	14.8	298 1	ADT3_HUMAN
11	365	14.7	357 1	LEU5_YEAST
12	360	14.5	298 1	ADT2_MOUSE
13	359	14.5	298 1	ADT2_HUMAN
14	358	14.4	298 1	ADT2_RAT
15	355.5	14.3	386 1	ADT1_SOLTU
16	355.5	14.3	387 1	ADT1_MAIZE
17	355	14.3	298 1	ADT1_MOUSE
18	355	14.3	298 1	ADT1_RAT
19	354.5	14.3	387 1	ADT2_MAIZE
20	354	14.3	305 1	ADT_KULULA
21	353.5	14.2	309 1	ADT1_YEAST
22	352	14.2	298 1	ADT1_HUMAN
23	352	14.2	339 1	ADT_CHUKE
24	351.5	14.2	318 1	ADT2_YEAST
25	350.5	14.1	382 1	ADT2_ORYSA
26	349.5	14.1	386 1	ADT1_GOSHI
27	348	14.0	297 1	ADT1_BOVIN
28	346.5	13.9	331 1	ADT1_WHEAT
29	346	13.9	385 1	ADT2_ARATH
30	345	13.9	313 1	ADT_NEUCR
31	344	13.9	381 1	ADT1_ARATH
32	341.5	13.8	331 1	ADT2_WHEAT
33	340	13.7	322 1	ADT2_SCHPO

34	339.5	13.7	307 1	ADT3_YEAST	P18238 saccharomyc
35	337	13.6	301 1	ADT2_ANOGA	O27238 anopheles g
36	337	13.6	386 1	ADT2_SOLTU	P27081 solanum tub
37	330.5	13.3	287 1	ADT2_DROME	O26365 drosophila
38	326.5	13.2	308 1	ADT1_CHLRE	P27080 chlamydomon
39	322.5	13.0	322 1	SEFC1_YEAST	P33303 saccharomyc
40	318	12.8	314 1	YG20_YEAST	P53237 saccharomyc
41	314.5	12.7	315 1	MFT_HUMAN	O9h281 homo sapien
42	311	12.5	695 1	CMC1_DROME	O9va73 drosophila
43	303.5	12.2	373 1	YIA6_YEAST	P4056 saccharomyc
44	295.5	11.9	702 1	CMC1_CAEEL	O21153 caenorhabd1
45	295	11.9	320 1	DNC_HUMAN	O9h221 homo sapien

## ALIGNMENTS

RESULT	ID	CMC2_CAEEL	STANDARD:	PRT:	588 AA.
AC	O20799:	CMC2_CAEEL			
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Probable calcium-binding mitochondrial carrier F55A11.4.				
GN	F55A11.4.				
OS	Caenorhabditis elegans.				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;				
OC	Rhabditidae; Peloderinae; Caenorhabditis.				
OX	NCBI_Taxid=6239;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-BRISTOL NZ;				
RA	Kershaw J.;				
RL	Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: CALCIUM-DEPENDENT MITOCHONDRIAL SOLUTE CARRIER (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL.				
CC	-1- INNER MEMBRANE (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. ARALAR SUBFAMILY.				
CC	-1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
DR	EMBL: Z72511; CAA96658.1; -				
DR	WormPep: F55A11.4; CE05946.				
DR	InterPro: IPR002048; EF-hand.				
DR	InterPro: IPR002067; MLC_carrier.				
DR	InterPro: IPR001993; Mitoch_carrier.				
DR	Pfam: PF00036; efhand; 3				
DR	Pfam: PF00153; mito_carr; 3.				
DR	PRINTS: PR00926; MITOCARRIER.				
DR	SMART: SM00054; Efh; 3.				
DR	PROSITE: PS00018; EF_HAND; 2.				
DR	PROSITE: PS00215; MITOCH_CARRIER; FALSE NEG.				
KW	Hypothetical protein: Mitochondrion; Inner membrane; Repeat;				
KW	Transmembrane; Transport; Calcium-binding.				
FT	TRANSMEM 252				
FT	TRANSMEM 269				
FT	TRANSMEM 307				
FT	TRANSMEM 352				
FT	TRANSMEM 365				
FT	TRANSMEM 403				
FT	TRANSMEM 446				
FT	TRANSMEM 463				
FT	TRANSMEM 504				
FT	CA_BIND 52				
FT	CA_BIND 86				
FT	DOMAIN 123				
FT	ANCESTRAL CALCIUM SITE 3.				

FT	CA BIND	153	164	EF-HAND 4.
FT	DOMAIN	189	535	3 APPROXIMATE TANDEM REPEATS
FT	REPEAT	189	335	1.
FT	REPEAT	326	429	2.
FT	REPEAT	430	535	3.
SO	SEQUENCE	588 AA:	66336 MM;	6ADDF60923D8697D CRC64;

Query Match	44.5%;	Score 1103;	DB 1;	Length 588;
Best Local Similarity	45.7%;	Pred. No. 1.9e-04;		
Matches 210;	Conservative 104;	Mismatches 142;	Indels 4;	Gaps 3;

QY	19	EÖPRLYEYELFÖALDRNDSQVVDIELOEGJRNLCIFPGOAAEKEIFTTGVNNDKIDEE	78
Db	73	EKEQOIRDIYRDLRIDNDGTIDIDIDLALKHEPHRPHILPAULAVIYNSKMSRPDEGVRDVF	132
QY	79	EPMKYLDKEHKMKLAFKSLDKDNNGKIEASEIVOSIQTULGTTISFOAELLQSIDVDG	138
Db	133	SFSSVYLENEOKLAEFMFADMDRNDHGDVDAVEMKNYCKSDIGVPLDHBKAOHYNNKKMDTG	192
QY	139	TMTYDMMNMRUYELFENVTDEELIIRWPKHSTGIDIGDSLITIDDEFEDKKSQGMWRQD	198
Db	193	SASVDLKEFOEFEMALYFPSSDLDKIDVDEWRNHLIJDIGESQIDPEDESQOMÖGIMMRHL	252
QY	199	LAGGIAGAVSRTSTAPDLRLKIRIMQVIGSKSDKKNITFGFEROWKKEGJISLWRNGTNY	258
Db	253	VAGGAGAVSRTCTAPDRKIKVYLQVYNSKTRNLRGVMSCLKLHABGIKSPWRGNOINV	312
QY	259	IKIAPETAVKRWALVEYQKKLLTEE--GÖKIGTPEPRFTSSGMAQATQFTIYPMENYKTRL	316
Db	313	IKIPEESIKRMCYDOLKRLDÖKKKEEISTEERLACGASAAALISOSTIYPMENYKTRL	372
QY	317	AVGTGTGYS--GIYUCAKKILKEHGLGAFYGYVYNLGIIPYAGIDILAVYELLSKSWLDN	375
Db	373	ALRTGTQDGRDRIIFHAKMKTKEBIRCFYGYGLPDLGIITPYAGIDALIVETLKRYYVR	432
QY	376	FAKDSVGNVALLCGCALSTGQOLASYPYLAIVRTMQAOAMLEGGSPOLN--WVGLFRRT	434
Db	433	YETNSSEGVYALLACGCSSTGOLSTSSYPALVTRTQALSTIRYSPQDITMGOFOKTYI	492
QY	435	ISKEGIDPLRGITPMPKUYLPAGISIVYVYENNKQYLG	474
Db	493	LÖNBEVGTGYRGITPMPKUYLPAGISIVYVYENNKQYLG	532

CC	RESULT	2			
CC	CMC3_CAEBL				
CC	ID	CMC3_CAEBL	STANDARD:	PRT:	587 AA.
CC	AC	Q19529;			
CC	DT	16-OCT-2001 (Rel. 40, Created)			
CC	DT	16-OCT-2001 (Rel. 40, Last sequence update)			
CC	DT	16-OCT-2001 (Rel. 40, Last annotation update)			
CC	DE	Probable calcium-binding mitochondrial carrier F17E5.2.			
CC	GN	F17E5.2.			
CC	OS	Caenorhabditis elegans.			
CC	OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;			
CC	OC	Rhabditidae; Pelodierinae; Caenorhabditis.			
CC	OX	NCBI_TaxID=6239;			
CC	RN	(1)			
CC	RP	SEQUENCE FROM N.A.			
CC	RC	STRAIN=BRISTOL N2;			
CC	RA	McMurray A.A.;			
CC	RL	Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.			
CC	CC	-1- FUNCTION: CALCIUM-DEPENDENT MITOCHONDRIAL SOLUTE CARRIER (BY SIMILARITY).			
CC	CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).			
CC	CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. ARLAR SUBFAMILY.			
CC	CC	-1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.			
CC	CC	-----			
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR	Embry; 230873; CA90701.27.	
DR	WormPep; F17E5.2; CE23667.	
DR	InterPro; IPR002048; EF-hand.	
DR	InterPro; IPR002047; Mt_carr.	
DR	InterPro; IPR001993; Mitocoh_carr.	
DR	Pfam; PF00036; efhand; 3.	
DR	Pfam; PF00153; mito_carr; 3.	
DR	PRINTS; PRO0526; MITOCARRIER.	
DR	SMART; SM00054; EFH; 2.	
DR	PROSITE; PS00018; EF_HAND; 2.	
DR	PROSITE; PS00215; MITOCH_CARRIER; FALSE_NEG.	
KW	Hypothetical protein: Mitochondrion; Inner membrane; Repeat.	
KW	Transmembrane; Transport; Calcium-binding.	
FT	TRANSMEM	265 .. 282
FT		1 (POTENTIAL).
FT	TRANSMEM	337 .. 356
FT		2 (POTENTIAL).
FT	TRANSMEM	382 .. 395
FT		3 (POTENTIAL).
FT	TRANSMEM	433 .. 452
FT		4 (POTENTIAL).
FT	TRANSMEM	475 .. 492
FT		5 (POTENTIAL).
FT	TRANSMEM	534 .. 551
FT		6 (POTENTIAL).
FT	CA_BIND	49 .. 60
FT		EF-HAND 1.
FT	CA_BIND	83 .. 94
FT		EF-HAND 2.
FT	DOMAIN	119 .. 129
FT		ANCESTRAL CALCIUM SITE 3.
FT	CA_BIND	149 .. 160
FT		EF-HAND 4.
FT	DOMAIN	185 .. 563
FT		3 APPROXIMATE TANDEM REPEATS.
FT	REPEAT	185 .. 365
FT		1.
FT	REPEAT	366 .. 459
FT		2.
FT	REPEAT	460 .. 563
FT		3.
SQ	SEQUENCE	587 AA; 65306 MW; 19E62936D5A17021 CRC64;

Query Match	39.8%;	Score 988.5;	DB 1;	Length 587;
Best Local Similarity	42.3%;	Pred. No. 5e-57;		
Matches 202;	Conservative 91;	Mismatches 137;	Indels 47;	Gaps 8;

OY	19	BOPTPEYELFCALBNGGVDVDELOEGJLNLGIPRGDAEKKIPLTGGVNMKGKIDFE	78
Db	70	EKEKIRDMYDRLDANDNGSIDIRDLQAL-SLOAHIPASVAPRLERMSSEHSDBVTYA	128
OY	79	EPMKYIKCHEKKMKIARSLDKNNDKGKIEASEIYOSIQTLGTLISBOAEILIOSIDVCG	138
Db	129	DFTNVIVAEHARLAEVEPKIDILNDSDEGDVAIEIKSYCEKMGVNLDDOKAMSYKKMDQSG	168
OY	139	TMIVDMNMRAPYLPFNPTDIEELIRFPKHSBTG-----IDIGDSLTP	181
Db	189	SSSVNLNEFQDFMLLYPSTDKMDVDFVRKMLVOTCESNSRFTQNFQIIDIIGEDQVR	248
OY	182	DETEDEKRSQOMWRQOLLAGSIAGAVSFTSTAPDLRLKI-----MMOY	224
Db	249	EDFPQOELLISGVMMRHLIAGVAGVAMSGSTCAPEDRIKIVLYQVWYLIHLFHEIMELKALQV	308
OY	225	HGMSDKNNINGGRFOWMKEGGISLWNGNTNVIKIAPEYAVYEMAYEQYKKLIE--E	282
Db	309	NSTKTKRIGVSVCHLLBAEGGISFEMGNSINVIKIIIPASAMKEMCYDQIKRMOYKQ	366
OY	283	GOKITFERFISGMAGATAQTFIYPRMEVMTRLAVAKTCQY--SGIADCAKKILIKHEGLG	341
Db	369	GAEIISTIERLLAGSSAGAIISOTAIYPRMEVMTRLALRTQGLDKGMHFRHMKYTKGKIK	428
OY	342	AFYKGYVNLIGIIPYAGIDILAVYELLSKWLNDNFAKDSVNPQVYMLLSCGALSSTGOL	401
Db	429	CFYKYUPLNLLGIIPYAGIDILTVESLSKSWY--TKYUTEHEPGLVALIACGSCSTGOL	487
OY	402	ASYPALVIRTMQAMQAMLESGPOLM-----WVGLFRRLIKKEGIPGLYRGITPPEMK	453
Db	488	ASYPALVIRTLQARAI--SPKNSSTOPDWNQGFKHILLOEGGTGLYRGITPPEMK	511



RESULT 3  
CMCL\_YEAST STANDARD: PRT: 545 AA.  
AC P48233:  
DT 01-FEB-1996 (rel. 33, Created)  
DT 16-OCT-2001 (rel. 40, Last sequence update)  
DT 16-OCT-2001 (rel. 40, Last annotation update)  
DE Probable calcium-binding mitochondrial carrier YNL083W.  
GN YNL083W OR N2312.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-S288C / FY1679;  
RX MEDLINE-96310628; PubMed-8740422;  
RA Soler-Mira A., Salz J.E., Ballesta J.P.G., Remacha M.;  
RT "The sequence of a 17,933 bp segment of Saccharomyces cerevisiae  
RT chromosome XIV contains the RHO2, TOP2, MKT1 and END3 genes and five  
RT new open reading frames."  
RL Yeast 12:485-491(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-S288C / FY1679;  
RX MEDLINE-96267764; PubMed-8701611;  
RA Pohlmann R., Philippsen P.;  
RT "Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome XIV  
RT reveals 12 new open reading frames (ORFs) and an ancient duplication  
RT of six ORFs."  
RL Yeast 12:391-402(1996).  
RN [3]  
RP REVISIONS TO C-TERMINUS.  
RX MEDLINE-97321806; PubMed-9178508;  
RA Moudilj B., Duyckaerts C., Lamotte-Brasseur J., Sluse F.E.;  
RT "Phylogenetic classification of the mitochondrial carrier family of  
RT Saccharomyces cerevisiae."  
RL Yeast 13:573-581(1997).  
CC -! FUNCTION: CALCIUM-DEPENDENT MITOCHONDRIAL SOLUTE CARRIER (BY  
CC SIMILARITY).  
CC -! SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC inner membrane (potential).  
CC -! SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. ARALAR  
CC SUBFAMILY.  
CC -! SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.  
CC -! CAUTION: REF.1 AND REF.2 SEQUENCES DIFFER FROM THAT SHOWN DUE TO A  
CC FRAMESHIFT IN POSITION 403.  
CC -----  
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CC -----  
DR EMBL: X89016; CAA61427.1; ALT\_FRAME.  
DR EMBL: 271359; CAA95958.1; ALT\_FRAME.  
DR SGD: S0005027; YNL083W.  
DR InterPro: IPR002048; EF-hand.  
DR InterPro: IPR002067; Mt\_carrier.  
DR InterPro: IPR001993; Mitoch\_carrier.  
DR Pfam: PF00036; efhand. 3.  
DR Pfam: PF00153; mito\_carr. 3.  
DR PRINTS: PR00926; MITOCARRIER.  
DR PROSITE: PS00018; EF\_HAND. 1.  
DR PROSITE: PS00215; MITOCH\_CARRIER. 1.  
KW Hypothetical protein; Mitochondrion; Inner membrane; Repeat;  
KW Transmembrane; Transport; Calcium-binding.  
FT TRANSMEM 231 248 1 (POTENTIAL).  
FT TRANSMEM 307 326 2 (POTENTIAL).  
FT TRANSMEM 355 368 3 (POTENTIAL).  
FT TRANSMEM 409 428 4 (POTENTIAL).

FT TRANSMEM 458 475 5 (POTENTIAL).  
FT TRANSMEM 516 535 6 (POTENTIAL).  
FT CA\_BIND 59 70 EF-HAND 1.  
FT CA\_BIND 93 104 EF-HAND 2.  
FT DOMAIN 127 136 ANCESTRAL CALCIUM SITE 3.  
FT CA\_BIND 155 166 EF-HAND 4.  
FT DOMAIN 191 545 3 APPROXIMATE TANDEM REPEATS.  
FT REPEAT 191 335 1.  
FT REPEAT 336 435 2.  
FT REPEAT 436 545 3.  
SQ SEQUENCE 545 AA: 61224 MW: B00C2309AE759AA9 CRC64;  
  
Query Match 24.6%; Score 611.5; DB 1; Length 545;  
Best Local Similarity 28.3%; Pred. No. 1.3e-32;  
Matches 155; Conservative 107; Mismatches 190; Indels 95; Gaps 15;  
  
OY 15 CQ-DADQPTREYETLFDALDRNGDGVDDIGELQGLRMIGIPL--GQDAEKKIFTGDYVK 71  
DB 6 CERDKQDRIDRYACLPKELDYKNGQVTLDMLIQAFENKDHPLKGNDAIKMLFTAMDYVK 65  
  
OY 72 DGLDFEPEPKYLLKDEKKMKLAFKSLDKNNDKIEASEI---VQSLQTLGLTISEQAE 128  
DB 66 DSVYDLSDFKKYASNAESQIWMNGFORDIDLDHDKIGINEINRYLSDLDNQSICNNELNHE 125  
  
OY 129 LIIQSID-----VDGTMVDNNEWRDYF 151  
DB 126 LSNKKVKKTSRFFEWAPPKRKANIALRGQASHKKNFDNDRSKTTSDDLYVYDQWDFL 185  
  
OY 152 LFNPDVNDIEET---IRFWKSTGIDT---GDSLTIPDEFTEDEKSGQWROLLAGIA 204  
DB 186 LLYPRKQGSRLHTAYSYFLFNEDVDLSSGCD-VTLINDT-----RQGFPIAGIS 237  
  
OY 205 GAVSRSTAPLRLKIMQVH-----GSKSDKM-----NIFGFPQMK 243  
DB 238 GVISRCTAFEDRLKFLARTDLSLILNSKTDLLAKNNADINKISSPLAAVKKLYR 297  
  
OY 244 EGGIRSLMRNGNINVIKIAETFRFMYEQYKILTE-BG-----QKIGFERRISGMA 298  
DB 298 QGGIRKAFYVGNGLNVIKVPESSTIKFGSEFYTKIMKLKSGCRDTKLSFSTIYAGLA 357  
  
OY 299 GATAGTFIYPMEMKTRLAGV---KTGYSGYDCAKKILKEGLGAFKGYVPNLGI 354  
DB 358 GMAAQSVYDIDILKFRVQCAPLDTKLKGNLLFQFAKDMFREGVALFYRGVYVIGI 417  
  
OY 355 ITPAGIDLAVYELKSTWLD-----NFAKDSVNPQVMVLGGGALSTGQGLASPLAL 408  
DB 418 FPYAALDLGTFSPALKRWYIAKQAKTLNLPQDOVTLNVLVLPMAFGFVGASVYVPI 477  
  
OY 409 VTRFMQAQMLBESSPOLN-MVGLFRIRISKEGIPGLYRGITPMPKVLPAVGSIVYVEN 467  
DB 478 LKTRRLQAQGYAHPIYVYNGFKVDLKTLEREGYQGLKGLVPTLAKVPAVSISYLCYEN 537  
  
OY 468 MKQTLGV 474  
DB 538 LKKFMNL 544  
  
RESULT 4  
GDC\_BOVIN STANDARD: PRT: 330 AA.  
ID GDC\_BOVIN  
AC G01888:  
DT 01-APR-1993 (rel. 25, Created)  
DT 01-APR-1993 (rel. 25, Last sequence update)  
DT 01-MAR-2002 (rel. 41, Last annotation update)  
DE Grave's disease carrier protein (GDC) (Mitochondrial solute carrier  
DE protein homolog).  
GN SLC25A16 OR GDA OR GDC.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;

Query Match	Best Local Similarity	19.4%	Score 480.5	DB 1	Length 330
Matches 112	Conservative 54	Mismatches 109	Indels 19	Gaps 8	
QY 194	WWRQLLAGGIAGAVSRTSTAPLDRIKIMQVHGSKDKNIFGGRVYKKEGSIKSLMWG	253			
Db 34	WLRSLFAGGIAGCCAKTTPVARDVRYKTLQAHNNHYRLHGVSTLRAPVKKRGYGLYKVG	93			
QY 254	NGTNIYIKIAPETAVKFAVMEYQKKLLTLEGCKITGFFERFISSMAGATPOTIYYMEYVK	313			
Db 94	NGAMMIRIFEPYGAIDFMFAFEHYKTLITTKLGVSHVHRLMASMGMPADVICITPDLMDVR	153			
QY 314	TRLAIVGKKYGO--YSGIYICCAKKILKHEG--LGAIFYKYGVVNNLGIITPYAGIDLAIVYELIK	369			
Db 154	VRLAQVYGEHNTYTGIIHAFKITVAKBEGFLG-FYRGMLPTILGNAPYAGVSEFFFEFGTLK	212			
QY 370	SWYLDNEFA-----KDSVNPQVYVL-----LCCGLALSTCGOLASTPLALVNTFRQADAM	418			
Db 213	SVGLT--STAPTLTGRSSDNPVLYLTKHINLLCGGVAGAIQVITISYPRDVTERRRQLGAV	271			
QY 419	L-EGSPOLNMVGLFRRITISKEGI-DGLVRGIPPNPMKVLPAVGISYVYUENKKO	470			
Db 272	LPEFEKCLMRETKMYVYVGHGIRKGLYRGISLNTIRCVPSQVAVAFITYELMKO	325			
RESULT 5					
ID GDC_HUMAN	STANDARD:	PRF:	332 AA.		
AC PI6260:					
DT 01-AUG-1990 (Rel. 15, Created)					
DT 01-JUL-1993 (Rel. 26, Last sequence update)					

Query Match	18.3%	Score 454.5;	DB 1;	Length 332;
Best Local Similarity	36.0%;	Pred. NO. 1.1e-22;		
DT	16-OCR-2001 (Rel. 40, Last annotation update)			
DE	Grave's disease carrier protein (GDC) (Grave's disease autoantigen)			
DE	(GDA) (Mitochondrial solute carrier protein homolog).			
GN	SLC25A16 OR GDA.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Thyroid;			
RX	MEDLINE=90114217; PubMed=25755220;			
RA	Zarrilli R., Oates E.L., McBride O.W., Lerman M.I., Chan J.Y.,			
RA	Santisteban P., Ursini M.V., Notkins A.D., Kohn L.D.;			
RT	"Sequence and chromosomal assignment of a novel cDNA identified by			
RT	immunoscreening of a thyroid expression library: similarity to a			
RT	family of mitochondrial solute carrier proteins.";			
RL	Mol. Endocrinol. 3:1498-1508(1989).			
RN	[2]			
RP	REVISONS TO C-TERMINUS.			
RX	MEDLINE=93091248; PubMed=1457817;			
RA	Fiermonte G., Runswick M.J., Walker J.E., Palmieri F.;			
RT	"Sequence and pattern of expression of a bovine homologue of a human			
RT	mitochondrial transport protein associated with Grave's disease.";			
RL	DNA Seq. 3:71-78(1992).			
RN	[3]			
RP	FUNCTION, AND SUBCELLULAR LOCATION.			
RX	MEDLINE=21106356; PubMed=11189296;			
RA	Prohl C., Pelzer W., Diekert K., Kmitya H., Bedekovics T., Kispal G.,			
RA	Lill R.;			
RT	"The yeast mitochondrial carrier leu5p and its human homologue Graves'			
RT	disease protein are required for accumulation of coenzyme A in the			
RT	matrix.";			
RL	Mol. Cell. Biol. 21:1089-1097(2001).			
CC	-1- FUNCTION: Required for the accumulation of coenzyme A in the			
CC	mitochondrial matrix.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial			
CC	inner membrane.			
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.			
CC	-1- DISEASE: POSSIBLE ROLE IN GRAVES' DISEASE. THIS PROTEIN IS			
CC	RECOGNIZED BY IGG FROM PATIENTS WITH ACTIVE GRAVE'S DISEASE.			
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.			
CC	-1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 320			
CC	ONWARD DUE TO A FRAMESHIFT.			
CC	-----			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; M31659; AAA36329.1; ALT_FRAME.			
DR	PIR; A40141; A40141.			
DR	MIM; 139080;			
DR	InterPro: IPR002067; Mit_carrier.			
DR	InterPro: IPR001993; Mitoch_carrier.			
DR	Pfam: PF00153; mltcarr; 3.			
DR	PRINTS; PR00926; MITOCARRIER.			
DR	PROSITE; PS00215; MITOCH_CARRIER; 3.			
KW	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.			
FT	TRANSMEM 134 154 POTENTIAL.			
FT	TRANSMEM 191 211 POTENTIAL.			
FT	TRANSMEM 234 254 POTENTIAL.			
FT	REPEAT 1 123 1.			
FT	REPEAT 124 219 2.			
FT	REPEAT 220 332 3.			
SO	SEQUENCE 332 AA; 36235 MW; CFDB8F4F3E7F0F4B CRC64;			



SQ SEQUENCE 436 AA: 46627 MW: 9600C05F603E9DAE CRC64:

Query Match 17.2%: Score 425.5; DB 1; Length 436;

Best Local Similarity 34.8%: Pred. No. 1.2e-20; Mismatches 105; Conservative 65; Indels 23; Gaps 9;

185 TEDEKSGQWNR---OLLAGGIAGAVSRRTSTAPLDRLKIMQVHSGSKDKNNIFGFRQ 240  
 121 SEPEGGQGDQDPAPARIVSGAIVASRTFVAPLETIRTHLMVSGIGDSM--AGVFW 178  
 241 MKKEGINSIMNGNKTNIKIPETAVKFWAEQYKILLTEGQ---KIGTERFISGM 297  
 179 IMQNGWGTGLFRGNVNVIVRAVPSKAIEHFTYDTAKKFLTPGDDEPKPIPTPIVAGAL 238  
 298 AGATQOTFIPMEWKTRLAVGKTQSGIYDCAKKILKEIGAFYKGVNLLGIIFY 357  
 239 AGFASTLCYPMELIKRTYTIK--DYIDNVAAIAFYKILDEPSELYRGLTSLIGVRY 297  
 358 AGIDLAVYELLKSYWLDNFAK--DSVNPGVWLLG--CGALSTGOLASYPALVTR 412  
 298 AACNFYAVETTLKRLYRATGRRGADVGVATLLIGSAGAIASS---ATPEPLEVARQ 353  
 413 MQAQMLESPPOL--NMGLFRRITSKEGIPGLYRITPNPKVLPAVGSIVYVENMKQ 470  
 354 MGVAV--GGROYONVLAHYCIILKEGAGLYRGLGSPCIKIMPAGIAFMYEACK 411  
 471 TL 472  
 412 IL 413

RESULT 8  
 YE08\_SCHPO STANDARD: PRT: 326 AA.

AC 013805; Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Putative mitochondrial carrier C17H9.08.  
 GN SPAC17H9.08.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RA Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.,  
 RL Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane (Potential).  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 CC  
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 CC  
 CC EMBL: 298597; CAB1217.1; -  
 DR InterPro: IPR002067; Mit\_carrier.  
 DR InterPro: IPR001993; Mitoch\_carrier.  
 DR Pfam: PF00153; mito\_carr; 3.  
 DR PRINTS: PR00926; MITOCARRIER.  
 DR PROSITE: PS00215; MITOCH\_CARRIER; 2.  
 KW Hypothetical protein: Mitochondrion; Inner membrane; Repeat;  
 KW Transmembrane; Transport.  
 FT TRANSMEM 16 36 POTENTIAL.

FT TRANSMEM 120 140 POTENTIAL.  
 FT TRANSMEM 191 211 POTENTIAL.  
 FT TRANSMEM 240 260 POTENTIAL.  
 FT TRANSMEM 294 314 POTENTIAL.  
 SQ SEQUENCE 326 AA: 37059 MW: 12163A73260F35D2 CRC64:

Query Match 15.8%: Score 392; DB 1; Length 326;  
 Best Local Similarity 29.7%: Pred. No. 1.2e-18;  
 Matches 94; Conservative 60; Mismatches 121; Indels 42; Gaps 7;

190 KSGQWRQLLAGIGAGVSRSTAPLDRLKIMQVH-----GSKDKNIFGFRQMYKE 244  
 19 KSG-----IAGTAGCAVAKSVAPLDKRLIYQNHASRYAVSRHLYAKAHYHV 72  
 245 GSIRSLRNGNINVIKIPETAVKFWAEQYKILLTEGQKIGTERFISGMAGTAOT 304  
 73 YGLHGIQGHITATLVKRVFYAGIKFVAYEVOYRVILRDEPETHARRFLSGSLAGTGSVF 132  
 305 FIYPMEMKTRLA-VKGTQYSGIYDCAKKIL-----KHEGIGA-----FYKGV 348  
 133 FYPLELIRIVRLAYITNTGKNPTLVQVTKDIFHERDFLCNKYPGLSRLSKICNFYRGS 192  
 349 PNLGLIIPAGIDLAVYELLKSYWLDNFAKDSVNPGVWV-----LGGALST 397  
 193 VTLTGIFFPAGMSFLAYDLA---TDFEHOKIDEMWSTKSKDKLKTWPELLCGAFAGV 248  
 398 GGLASYPALVTRPMQQAQMLEGSPOLNMGLFRRITSKEGIPGLYRITPNPKVLPA 457  
 249 CGQIVSYFPEVCRKRMQIGIRKNSFLRLKQVOVOTTYKEAGMRGFPVGLTIGYIKVIM 308  
 458 VGISYVYVENMKQTLGV 474  
 309 VSTSFVYVNHRSKALLGI 325

RESULT 9  
 ADT3\_BOVIN STANDARD: PRT: 298 AA.

AC P32007; Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE ADP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine  
 DE nucleotide translocator 3) (ANT 3).  
 GN SLC25A6 OR ANT3.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89229093; PubMed=2540808;  
 RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;  
 RL "Two bovine genes for mitochondrial ADP/ATP translocase expressed  
 RL differences in various tissues."; Biochemistry 28:866-873(1989).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 CC  
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CC -----
DR EMBL: M24103; AAA30769.1; -.
DR PIR: B43646; B43646.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KM Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport;
KM Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 2 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DF6EDE4061 CRC64;

Query Match 14.8%; Score 369; DB 1; Length 298;
Best Local Similarity 32.3%; Pred. No. 3.5e-17;
Matches 96; Conservative 62; Mismatches 111; Indels 28; Gaps 10;

OY 196 ROLLAGGAGAVSRSTAPLDRLKIMOV-HGSK---SDKM--NIFGFRQWKEGIRS 249
DB 10 KPLAGGIAAIASTKTAAPLERVKLLQVOHASQIAADKQYKGYDCIVRIPEGVLS 69
OY 250 LMRNGNTNVIKIAPETAFAVWAEYQYKKLLTEEGOKIGTFERFISGSM---AGATAQT 304
DB 70 FWRGNLANVIRFPQALNFAFKDKKQIFLGVDKRTQFWRFAGNLASGGAAGATSLC 129
OY 305 FIYPMEMKTRLA--VGKTG---QYSGIYDCAKKILKHEGLAFYKYVNLGIIIPYAG 359
DB 130 FVYPLDFARTRLAADVGKSGSEREFRLGDLVKIRKSGIRGLYOGFVNSVOGIIITYRA 189
OY 360 IDLAVYELLSYWLDFNFAKDSVNPWGAVLLGCGALSTGQGLASYPALVYRTFMQAQML 419
DB 190 AVEGVIDTAK-----GMLDPKNTHTIVSWMIAQVYTAAGVSYSPDVTYRRMMQSGR 244
OY 420 EGSPOI--NMVGLFRRIRISKEGIPGLYRTFPMKVLPAVGISY--VVEYNNKQTL 472
DB 245 KGADIMYKGTVCQMKRIILKDEGKKAFFKAMSN---VLNGMGAFVLYLDELKVIY 298

RESULT 10
ADT3_HUMAN STANDARD; PRT; 298 AA.
ID P12336; O96C49;
AC 01-OCT-1988 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
DE (Adenine nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89236396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RL ADP/ATP translocase."
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

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RN [3]
RP SEQUENCE OF 36-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Actardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC - FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC - SUBUNIT: HOMODIMER.
CC - SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC - DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: J03592; AAA36750.1; -.
DR PIR: BC014775; AAH14775.1; -.
DR PIR: S03894; S03894.
DR PIR: B28116; B28116.
DR MIM: 300151; -.
DR MIM: 403000; -.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KM Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport;
KM Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 101 1.
FT REPEAT 101 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 105 108 KHTQ -> RHA (IN REF. 3).
FT CONFLICT 242 242 S -> F (IN REF. 2).
SQ SEQUENCE 298 AA; 32866 MW; 18534E9F0EA9672F CRC64;

Query Match 14.8%; Score 368; DB 1; Length 298;
Best Local Similarity 32.7%; Pred. No. 4e-17;
Matches 97; Conservative 60; Mismatches 112; Indels 28; Gaps 10;

OY 196 ROLLAGGAGAVSRSTAPLDRLKIMOV-HGSK---SDKM--NIFGFRQWKEGIRS 249
DB 10 KPLAGGIAAIASTKTAAPLERVKLLQVOHASQIAADKQYKGYDCIVRIPEGVLS 69
OY 250 LMRNGNTNVIKIAPETAFAVWAEYQYKKLLTEEGOKIGTFERFISGSM---AGATAQT 304
DB 70 FWRGNLANVIRFPQALNFAFKDKKQIFLGVDKRTQFWRFAGNLASGGAAGATSLC 129
OY 305 FIYPMEMKTRLA--VGKTG---QYSGIYDCAKKILKHEGLAFYKYVNLGIIIPYAG 359
DB 130 FVYPLDFARTRLAADVGKSGSEREFRLGDLVKIRKSGIRGLYOGFVNSVOGIIITYRA 189
OY 360 IDLAVYELLSYWLDFNFAKDSVNPWGAVLLGCGALSTGQGLASYPALVYRTFMQAQML 419
DB 190 AVEGVIDTAK-----GMLDPKNTHTIVSWMIAQVYTAAGVSYSPDVTYRRMMQSGR 244
OY 420 EGSPOI--NMVGLFRRIRISKEGIPGLYRTFPMKVLPAVGISY--VVEYNNKQTL 472
DB 245 KGADIMYKGTVCQMKRIILKDEGKKAFFKAMSN---VLNGMGAFVLYLDELKVIY 298

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DB 245 KGADIMYTGVDQWRIERDEGGKAFKGAWSN---VLRGMGAFVLVYDELKKVI 298

RESULT 11

LEU5\_YEAST STANDARD: PRT; 357 AA.

AC P38702;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Mitochondrial carrier protein LEU5.

GN LEU5 OR YHR002W.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI\_TaxID=4932;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=S288C / AB972;

RX MEDLINE=94378003; PubMed=8091229;

RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kueba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevisakis E., Vaughan K., Vignati D., Wilcox L., Woldman P., Waterston R., Wilson R., Vaudin M.;

RA "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome VIII.";

RT Science 265:2077-2082(1994).

RL [2]

RN FUNCTION, AND SUBCELLULAR LOCATION.

RX MEDLINE=21106356; PubMed=11158296;

RA Prohl C., Pelzer W., Diekert K., Knita H., Bedekovics T., Kispal G., Lill R.;

RA "The yeast mitochondrial carrier leu5p and its human homologue Graves' disease protein are required for accumulation of coenzyme A in the matrix.";

RT Mol. Cell. Biol. 21:1089-1097(2001).

CC -1- FUNCTION: Required for the accumulation of coenzyme A in the mitochondrial matrix.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

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CC -----

DR EMBL; U10555; AAB68424.1; -.

DR PIR; S46795; S46795.

DR SGD; S0001044; LEU5.

DR InterPro; IPR002067; Mit\_carrier.

DR InterPro; IPR001993; Mitoch\_carrier.

DR Pfam; PF00153; mito\_carr; 3.

DR PRINTS; PR00926; MITOCARRIER.

DR PROSITE; PS00215; MITOCH\_CARRIER; 3.

DR Mitochondrion; inner membrane; Repeat; Transmembrane; Transport.

FT TRANSMEM 136 153 POTENTIAL.

FT TRANSMEM 208 228 POTENTIAL.

FT TRANSMEM 325 347 POTENTIAL.

FT SEQUENCE 357 AA; 40825 MW; 16266b2CD4B99605 CRC64;

Query Match 14.7%; Score 365; DB 1; Length 357;

Best Local Similarity 30.1%; Pred. NO. 7.9e-17;

Matches 98; Conservative 55; Mismatches 123; Indels 50; Gaps 9;

OY 196 ROLLAGIAGAVSTRTAPDLRLKTMQV---HGSK--SDKNNIFGTRQWKEGCISSL 250

DB 35 RSLAGAGISGSCAKTLPIADLRKILFQTSNPHYKRYGSLGLWEAKHIMWNGKGF 94

OY 251 MRGNGTNVIAKIAPEFAVFWAEQYKKILLTEEGKIGTFEPIISGSMGATPQFIYME 310

DB 95 FQGHSAITLRIFFPAVAVFVAEQIRNLIIPSKFESHMRRLVSGSLGCSVFITPLD 154

OY 311 VKRTIYAVGKTQGYSGIYDCAKKILKEHGLGA-----FYKGYVNNLGI 354

DB 155 LVRAVLAEETEKRRVKLRILIKIYKEPASATLIKNDYIPNMFCHMCNFRGYPTVLGM 214

OY 355 IPYAGIDLAIVEL---LKSTW-----LDNFKADSYNP-GWAVLGCGLS 395

DB 215 IPYAGVSFFAHLDLHDVYKSPFFAPYSVLESEDDLERYVKORRPLRTMAELISGLLA 274

OY 396 STCGGLASVPLAVTRTRQAOAMLEGGSP-----OLNWNGLFRITISKE-GIPGLYRGIT 448

DB 275 GNASOTAAVPEETIRRLQVSAAL---SPKTYMDHKFOSISEIAHIIIEKRGYRGFFVGLS 331

OY 449 PNFMKVLPVAGISYVYENMKOTLCV 474

DB 332 IGYIKVTPVACSFPEYERMKWNFGI 357

RESULT 12

ADT2\_MOUSE STANDARD: PRT; 298 AA.

ID ADT2\_MOUSE

AC P51881; 061311;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)

DE (Adenine nucleotide translocator 2) (ANT 2).

GN SLC25A5 OR ANT2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=97059403; PubMed=8903724;

RA Ellison J.W., Li X., Francke U., Shapiro L.J.;

RA "Rapid evolution of human pseudautosomal genes and their mouse homologs.";

RT Mamm. Genome 7:25-30(1996).

RL [2]

RN SEQUENCE FROM N.A.

RP TISSUE=Skeletal muscle;

RA Sheldon J.G.;

RL Thesis (1995), University of Cambridge, U.K.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SV;

RA Costet P., Laplace C.;

RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.

RN [4]

RP REVISIONS.

RA Laplace C.;

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RX PubMed=10974536;

RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;

RA "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes.";

RL Gene 254:57-66(2000).

CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.

CC -1- SUBUNIT: HOMODIMER.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

```

CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U27316; AAC52838.1; -
DR EMBL: U10404; AAA19009.1; -
DR EMBL: X70847; CAA50196.1; -
DR EMBL: AF240003; AAF64471.1; -
DR MGD: MGI:1353496; SLC25A5.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SO SEQUENCE 298 AA; 32931 MW; 0798E04B987EFE20 CRC64;

Query Match 14.5%; Score 360; DB 1; Length 298;
Best Local Similarity 31.9%; Pred. No. 1.3e-16;
Matches 94; Conservative 60; Mismatches 113; Indels 28; Gaps 10;

OY 196 ROLLAGGAGVSRSTALDLRLKIMOV-HGSK---SRKM-NITGGRONWKEGIGS 249
DB 10 KQFLAGGVAALSKTAVNAIEYKLLLOVHASKITADKQYKIIDCVIRIPKEGIVLS 69
OY 250 LWRGNSTNVIKIAETAVFYAYEYOYKRLTEGOKIGTFEERFISGM-----AGATACT 304
DB 70 FMRGNLIANVIRFPQALFAFKDKTKQFLGCVDRKTFWIRFONLSGCAAGATSLC 129
OY 305 FIYPMEVMTRLA-VGKTG---QYSGIYDCAKKILHGBLGAFYKGYVNLGIIIPYAG 359
DB 130 FYYPIDFAFTRLADYGVKAGAREFGKGLDCLVYKKISDGKGLYGFVNSVOGIIITYRA 189
OY 360 IDLAVYELLSKTVLDNFADSVNPGVMVLLGCGALSTGQGLASTPLAVRTRMQAOML 419
DB 190 AVEGYIDAK-----GMLPDPKNTLFIISMIAOSYTAVAAGLISYFEDVRRMMQSGR 244
OY 420 EESPOL--NMVGLFRIIRIKEGIPGLYGTPEFMKVLPAVGISY--VYVENMKO 470
DB 245 KGTIDIMYGTLDCKWKRIARDEGSKAFKGMASN---VLGMGGAFLVLYDEIKK 296

RESULT 13
ADT2_HUMAN STANDARD: PRT; 298 AA.
AC P05141; O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

```

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
RT cloning and sequence.";
RL J. Biol. Chem. 265:16060-16063(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87166056; PubMed=3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT growth-regulated.";
RL J. Biol. Chem. 262:4355-4358(1987).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraia R.,
RA Mazarella R.A., Schlessinger D., Chen E.Y.;
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Becker M., Graves T., Ozersky P.;
RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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CC -----
DR EMBL: M57424; AAA51737.1; -
DR EMBL: J02683; AAA5579.1; -
DR EMBL: L78810; AAB39266.1; -
DR EMBL: AC004000; AAB96347.1; -
DR EMBL: J03591; AAA36749.1; -
DR PIR: A29132; A29132.
DR PIR: C28116; C28116.
DR MIM: 300150; -
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.

```







```
CC -! DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -! SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; X62123; CAA44054.1; -.
DR PIR; S17917; S17917.
DR PIR; S21974; S21974.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Transit peptide; Multigene family.
FT TRANSIT 1 77 MITOCHONDRION.
FT CHAIN 78 386 ADP,ATP CARRIER PROTEIN.
FT TRANSMEM 90 107 1 (POTENTIAL).
FT TRANSMEM 152 170 2 (POTENTIAL).
FT TRANSMEM 195 212 3 (POTENTIAL).
FT TRANSMEM 256 275 4 (POTENTIAL).
FT TRANSMEM 295 312 5 (POTENTIAL).
FT TRANSMEM 351 369 6 (POTENTIAL).
SQ SEQUENCE 386 AA; 42058 MW; 68223D27A0B4EFB0 CRC64;

Query Match 14.3%; Score 355.5; DB 1; Length 386;
Best Local Similarity 31.2%; Pred.No. 3.6e-16;
Matches 92; Conservative 55; Mismatches 117; Indels 31; Gaps 7;

QY 188 EKSSGQMWROLAAGTAVSRTSTAPLDRLKIMQVHSGSKSDKM-----NIFG 236
DB 80 EKGFAPATDFLMGVSAAVSKTAAPIERVKLLIQ-----NODEMLKAGRLSEPYKGIGE 135
QY 237 GFRQMYKEGGISLWRNGNTNVIKIAPEYAVKFWAYEQYKKLLTEGQKIGTFERF---- 292
DB 136 CEGRTIKKEGFGSLMRGNTANVIRYPTQALNFAFKDYFKRLFNFKKRDGYKWFAGNL 195
QY 293 ISGSMAGTAQGEIYPMETWKTPLA----VGKYG---QYSGIYDCAKKIKHGLGAFYK 345
DB 196 ASGGAAGASLSLFFVSLDYARTRLANDRKASKKGGERQENGLVDYKTKLTKSDGIAGLYR 255
QY 346 GYVPNLGIIPYAGIDLAVYELKSYWLDNFADSVNPGVMVLDGCGALSTGCOLASYP 405
DB 256 GFNISCVGLIIVRGLYFGWYDSKLPVLLTGNLQDS----FFASFGLGWLTITNGAGLASYP 311
QY 406 LALVTRMQAOAMLEGSPOLNMVGLFRRIISKEGIPGLYRGITPNFMKYLPAVGI 460
DB 312 IDTVRRMMMTSG-EAVVKYKSSLDAPFQIYKNEGPKSLFKGAGANILRAVAGAGV 365
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Search completed: August 18, 2002, 09:31:11  
Job time: 486 sec

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OM protein - protein search, using sw model

Run on: August 18, 2002, 09:22:25 ; Search time 69.46 Seconds  
(without alignments)  
1188.001 Million cell updates/sec

Title: US-09-777-921A-2  
Perfect score: 2481  
Sequence: 1 MLRWLRFALEPTACQDAEQ.....VGISVYVENKKQTIGVTQK 477

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp-archaea:\*  
2: sp-bacteria:\*  
3: sp-fungi:\*  
4: sp-human:\*  
5: sp-invertebrate:\*  
6: sp-mammal:\*  
7: sp-mhc:\*  
8: sp-organelle:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-rodent:\*  
12: sp-virus:\*  
13: sp-vertebrate:\*  
14: sp-unclassified:\*  
15: sp-rylous:\*  
16: sp-bacteriap:\*  
17: sp-archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2373	95.6	475	6	018757 Oryctolagus
2	2132	85.9	411	4	09P129 Oryctolagus
3	1518	61.2	473	11	09D565 Mus musculus
4	1487	59.9	568	4	096P21 Homo sapiens
5	1397	56.3	384	4	096N04 Homo sapiens
6	1285	51.8	482	4	09BV35 Homo sapiens
7	1110	44.7	311	4	09BSA6 Homo sapiens
8	902	36.4	370	5	09VTX3 Homo sapiens
9	885.5	35.7	487	10	09F1A3 Arabidopsis
10	852	34.3	479	10	09LY28 Arabidopsis
11	840	33.9	478	10	09FLS8 Arabidopsis
12	652	26.3	631	3	09HE62 Neurospora
13	612.5	24.7	545	3	096U51 Saccharomyces
14	521	21.0	352	10	004619 Oryza sativa
15	520	21.0	322	10	09F082 Oryza sativa
16	520	21.0	332	10	09M058 Arabidopsis

17	506	20.4	358	10	09M333 Arabidopsis
18	500.5	20.2	426	3	094502 Schizosaccharomyces
19	475	19.1	348	10	09SH98 Arabidopsis
20	462	18.6	126	11	099KD3 Mus musculus
21	455.5	18.4	415	10	09M024 Arabidopsis
22	454.5	18.3	381	10	065023 Arabidopsis
23	448	18.1	316	5	09NI37 Trichomonas
24	448	18.1	325	10	09S219 Arabidopsis
25	446	18.0	385	10	09ZNY4 Solanum tuberosum
26	446	18.0	382	10	09S0V1 Arabidopsis
27	445.5	18.0	381	10	09LD54 Arabidopsis
28	434.5	17.5	428	10	09LV81 Arabidopsis
29	429.5	17.3	294	5	093717 Caenorhabditis
30	425.5	17.2	418	10	09C9R4 Arabidopsis
31	417.5	16.8	326	3	012251 Saccharomyces
32	410.5	16.5	377	5	09VDL7 Arabidopsis
33	400.5	16.1	319	10	09MA27 Arabidopsis
34	371	15.0	298	13	09PRH1 Arabidopsis
35	369	14.9	339	10	09EF73 Arabidopsis
36	368	14.8	298	13	09PRH2 Arabidopsis
37	367.5	14.8	348	10	09LJX5 Arabidopsis
38	367	14.7	298	13	09ITC4 Arabidopsis
39	365	14.7	298	4	096C49 Homo sapiens
40	362.5	14.6	334	10	094222 Oryza sativa
41	360	14.5	298	13	09I9M9 Arabidopsis
42	359	14.5	301	5	025692 Plasmodium
43	357.5	14.4	346	10	09LIF7 Arabidopsis
44	356	14.3	301	5	026006 Plasmodium
45	355.5	14.3	315	4	09H0C2 Homo sapiens

## ALIGNMENTS

RESULT ID	1	PRELIMINARY	PRT	475 AA.
018757	018757			
AC	018757			
DT	01-JAN-1998 (TREMBL)	05, Created		
DT	01-DEC-2001 (TREMBL)	19, Last sequence update		
DE	PEROXISOMAL CA-DEPENDENT SOLUTE CARRIER.			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_Taxid=9986;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-97385133; PubMed-9238007;			
RA	Weber F.E., Minestrini G., Dyer J.H., Werdner M., Boffelli D.,			
RA	Compassi S., Wehrli E., Thomas R.M., Schultze G., Hauser H.;			
RT	"Molecular cloning of a peroxisomal Ca <sup>2+</sup> -dependent member of the			
RT	mitochondrial carrier superfamily."			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:8509-8514(1997).			
CC	-1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.			
DR	EMBL: AF004161; AAB69156.1; -			
DR	HSSP: P09860; 3CTN			
DR	InterPro: IPR002048; EF-hand.			
DR	InterPro: IPR001993; Mitoch_carrier.			
DR	InterPro: IPR002067; Mlt_carrier.			
DR	Pfam: PF00036; efhand; 4.			
DR	Pfam: PF00153; mito_carr; 3.			
DR	PRINTS: PRO0926; MITOCARRIER.			
DR	SMART: SM0054; EFh; 3.			
DR	PROSITE: PS00018; EF_HAND; UNKNOWN_3.			
KW	Calcium-binding.			
SQ	SEQUENCE 475 AA; 53006 MW; E779D43F7C758269 CRC64;			

Query Match 95.6%; Score 2373; DB 6; Length 475;  
Best Local Similarity 95.2%; Pred. No. 3.7e-170;  
Matches 454; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

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OY 1 MURWLDALPLPAACQDAEQPTRYETLFOALDRNGDVYDDELQELGNLGIPLGQDAE 60
Db 1 MURWLRGVPLPAACQGAEPPTRYETLFOALDRNGDVYDDELQELGNLGIPLGQDAE 60
OY 61 EKPIFTGVNKGKLDLDFEEMFKYLLDKHEKMKLAFKSLDKNNDKGLEASEIYQSLQTL 120
Db 61 EKPIFTGVNKGKLDLDFEEMFKYLLDKHEKMKLAFKSLDKNNDKGLEASEIYQSLQTL 120
OY 121 TISEQOAEILLQSIDADGTMVDMNEMRDYFLFNPVADIEELIRPMKSHSTGIDIGSLTI 180
Db 121 TISEQOAEILLQSIDADGTMVDMNEMRDYFLFNPVADIEELIRPMKSHSTGIDIGSLTI 180
OY 181 PDEFDEDEKSSQGMWROLLAGIAGAVSRTSTAPLDRKIMQVHGSKSDKNINIFGFRQ 240
Db 181 PDEFDEDEKSSQGMWROLLAGIAGAVSRTSTAPLDRKIMQVHGSKSDKNINIFGFRQ 238
OY 241 MKVEGISLWNGTNTYIKIAPETAVKFMAVEQYKKLITEGOKIGTFERRISGSMAGA 300
Db 239 MKVEGISLWNGTNTYIKIAPETAVKFMAVEQYKKLITEGOKIGTFERRISGSMAGA 298
OY 301 TAQPTIYMEVVKTRIAVAGTGOYSGIYDCAKKILKHEGLGAFYKGYVNLGIIIPYAGI 360
Db 299 TAQPTIYMEVVKTRIAVAGTGOYSGIYDCAKKILKHEGLGAFYKGYVNLGIIIPYAGI 358
OY 361 DLAVVELLAKSYLDNFADKDVNPVWLLGCGALSTGQGLASYPALVTRTMQAOAMLE 420
Db 359 DLAVVELLAKSYLDNFADKDVNPVWLLGCGALSTGQGLASYPALVTRTMQAOAMLE 418
OY 421 GSPOLNMYGLFRRITSKGIEPLGTYGTPNFMKVLPAVGISVYVENMKOTIGVOK 477
Db 419 GAPOLNMYGLFRRITSKGIEPLGTYGTPNFMKVLPAVGISVYVENMKOTIGVOK 475

RESULT 2
OY 09P129 PRELIMINARY; PRT; 411 AA.
AC 09P129.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CALCIUM-BINDING TRANSPORTER (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RETINA;
RA Biery B., Valle D.;
RT "Cloning and subcellular localization of a human calcium-binding
RT transporter."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF123303; AAF28888.1; -
DR HSSP: P09860; 3CTN.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carrier.
DR PRINTS: PR00926; MITOCARRIER.
DR SMART: SM00054; EFh_3.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_3.
FT NON_TER 1
SO SEQUENCE 411 AA; 45819 MW; 99A3B5BAD9C2A4CF CRC64;

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Query Match 85.9%; Score 2132; DB 4; Length 411;  
 Best Local Similarity 99.8%; Pred. No. 4e-152;  
 Matches 409; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 8 FALPFAACQDAEQPTRYETLFOALDRNGDVYDDELQELGNLGIPLGQDAEKKFTTG 67
Db 1 FALPFAACQDAEQPTRYETLFOALDRNGDVYDDELQELGNLGIPLGQDAEKKFTTG 60

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OY 68 DYNKKGKLDLDFEEMFKYLLDKHEKMKLAFKSLDKNNDKGLEASEIYQSLQTLTISEQOA 127
Db 61 DYNKKGKLDLDFEEMFKYLLDKHEKMKLAFKSLDKNNDKGLEASEIYQSLQTLTISEQOA 120
OY 128 ELILOSIDVDGTMVDMNEMRDYFLFNPVADIEELIRPMKSHSTGIDIGSLTIPEDETD 187
Db 121 ELILOSIDVDGTMVDMNEMRDYFLFNPVADIEELIRPMKSHSTGIDIGSLTIPEDETD 180
OY 188 EKKSQGMWROLLAGIAGAVSRTSTAPLDRKIMQVHGSKSDKNINIFGFRQWKEGGI 247
Db 181 EKKSQGMWROLLAGIAGAVSRTSTAPLDRKIMQVHGSKSDKNINIFGFRQWKEGGI 240
OY 248 RSLMRNGTNTYIKIAPETAVKFMAVEQYKKLITEGOKIGTFERRISGSMAGATQTFILY 307
Db 241 RSLMRNGTNTYIKIAPETAVKFMAVEQYKKLITEGOKIGTFERRISGSMAGATQTFILY 300
OY 308 PNEVVKTRIAVAGTGOYSGIYDCAKKILKHEGLGAFYKGYVNLGIIIPYAGIDLAVEL 367
Db 301 PNEVVKTRIAVAGTGOYSGIYDCAKKILKHEGLGAFYKGYVNLGIIIPYAGIDLAVEL 360
OY 368 LKSYLDNFADKDVNPVWLLGCGALSTGQGLASYPALVTRTMQAOA 417
Db 361 LKSYLDNFADKDVNPVWLLGCGALSTGQGLASYPALVTRTMQAOA 410

RESULT 3
OY 09D5G5 PRELIMINARY; PRT; 473 AA.
AC 09D5G5.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 4930443G12RIK.
GN 4930443G12RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schmitt L. M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F.,
RA Brownstein M. J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D. A., Kamliya M., Lee N. H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
RA Noriome P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata K., Storch K. F.,
RA Suzuki H., Toyooka K., Wang K. H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK015371; BAB29816.1; -
DR HSSP: Q64537; IDVI.
DR MGD: MGI:1921936; 4930443G12RIK.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR Pfam: PF00153; mito_carrier.
DR PRINTS: PR00926; MITOCARRIER.
DR SMART: SM00054; EFh_4.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
SO SEQUENCE 473 AA; 53375 MW; 6EF920A84651EB63 CRC64;

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OY	215	LDRKIMMOVHSSKSDKNMIEGCFQOMKEGGIRSLMRNGNNIVLKIAETVAEPKAYAO	274
Db	122	LDRLEPMOVHASKNRNLNLTGLSKSMVEEGEIRSLMRONGINVLKIAESAIFKPAYAO	181
OY	275	YKKLITEERGOKIGTERFISGSAGATAQTIFYPEWMTKRILAVGTQSGIYDCAKKI	334
Db	182	IKRALLTGOGEPLTHVERFVAGSLACATAGTIYPHEVLTKRLTLRTGTGYKGLLDCAARI	241
OY	335	LKHESLGAFYKYVPNLLGIPIPYAGIDLAUYELKLSYWLDNFAKDSVNDGVNVLGCAL	394
Db	242	LEREGRPAFRFYRGYLTPNVNLIIPYAGIDLAUYETKLNMWLOOQYSHPDADGIIIVLLACGTI	301
OY	395	SSTGOLASYPALVTRTHQAQMLEGSPQLMMVGIFRRILISEKGPJGRGITPMEKV	454
Db	302	SSTCGOLASYPALVTRTHQAQSIEGGFQSLMLGHLRIHSQEGRMGLRYGIAFNEMKV	361
OY	455	LPVAGISYVVVENMKOTLGVTOK 477	
Db	362	IPAVISYVVVENMKQALGVISR 384	
RESULT	6		
O9BV35			
ID	O9BV35	PRELIMINARY:	PRT: 482 AA.
AC	O9BV35:		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DI	HYPOTHETICAL 54.0 KDA PROTEIN.		
OC	Homo sapiens (Human).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.		
RN	NCBL Taxid=9606;		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=EYE, RETINOBLASTOMA;		
RA	Strausberg R.;		
RL	Submitted (Jan-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC001656; AAH01656.1; -		
DR	InterPro: IPR002048; EF-hand.		
DR	InterPro: IPR001993; Mitoch_carrier.		
DR	InterPro: IPR002067; Mlt_carrier.		
DR	Pfam; PF00163; mltc_carr_2.		
DR	PRINTS; PR00926; MITOCARRIER.		
DR	SMART; SM00054; EFh_3.		
DR	PROSITE; PS00018; EF_HAND; UNKNOWN_2.		
KW	Hypothetical protein.		
SO	SEQUENCE 482 AA; 54035 MW; 8917BBA2BC2FE42B CRC64;		
Query Match	51.8%; Score 1285; DB 4; Length 482;		
Best Local Similarity	53.7%; Pred. No. 2,6e-88;		
Matches 242;	Conservative 77; Mismatches 78; Indels 54; Gaps		
OY	17	DAEOGTRETYFLQALDRKGDGVVDIGELQGRNLGIPYGOD---AEKITTGTGVNKD	72
Db	7	DAERQRQRGRLEELDLSKDKGRVDVDELHQGLARLG--GGNPDDGAQGSISEGADPD	63
OY	73	GKLDEEPMKYKLDEKKMYKLAFKSLDKNNCKITKASEATVOSTGLTGILLTSIQOAFLIIQ	132
Db	64	GGLDEEFSSKRYLQEKORLLMFHSLDRNQDGHIDVSEIQOSFRALGISISLBQAEKLIH	123
OY	133	SIDVDGTTVDVMENWRDFLENPVTDIEBILRFMKHST-----	170
Db	124	SMDRDGTWTIDMQEWRDHFLHLSLNVEDVLYFMKHSTLSASGFSAWIKDSTAEDQRSKT	183
OY	171	-----GIDIGDSLTPDETTEDEKKSQGMWROLLAGTING	205
Db	184	TVLARSGSHLKSQHFGRRPKWADHEVLIDIGECTLYPDEFSSKOEKLTGMMWKOLVAGAVAL	243
OY	206	AVSRSTAPDLRLKIMQVHGSKSKMNIFGFRQMVYDGIRSLMRNGTNVIKIAPET	265
Db	244	AVSRGTAPDLRLKFMQVHGSKSKNTNLTGLRSNVTLEGGIRSLMRNGINVLKIADES	303

QY	AKFMAYQDYOKKLLLEEGOKIGTFERFISGSMAGATAQTFIEMVEMKTRILVNGKTOYS	325
Db	304 AKFMAYQDYOKKLLLEEGOKIGTFERFISGSMAGATAQTFIEMVEMKTRILVNGKTOYS	363
QY	326 GYDCAKRLILKEGGAFAFGKGYVPMILGIPYAGIDILAYEELKSWIDNFKDSVNPV	385
Db	364 GYDCAKRLILKEGGAFAFGKGYVPMILGIPYAGIDILAYEELKSWIDNFKDSVNPV	423
QY	386 MYLGGALISSTGGGLASTPLALVTRTMOAQ	416
Db	424 MYLGGALISSTGGGLASTPLALVTRTMOAQ	454
RESULT	7	
Q9BSA6	PRELIMINARY: PRT: 311 AA.	
AC	Q9BSA6: Q9BSA6:	
DT	01-JUN-2001 (TREMBLrel. 17, Created)	
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)	
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DT	HYPOTHETICAL 34.0 KDA PROTEIN (FRAGMENT).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
CC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
CC	NCBI_Taxid=9606;	
CK	(1)	
RN	SEQUENCE FROM N.A.	
RP	TISSUE=MUSCLE, RHABDOMYOSARCOMA;	
RC	Strausberg R.;	
RL	Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.	
DR	EMBL, BC005163; AAH05163.1; -	
DR	InterPro: IPR001993; Mitoch_carrier.	
DR	InterPro: IPR002067; Mit_carrier.	
DR	Pfam: PF00153; mito_carr; 3.	
DR	PRINTS: PR00926; MITOCARRIER.	
DR	PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_2.	
DR	Hypothetical protein.	
KW	NON_TER	
FT	SEQUENCE 311 AA; 33991 MW; 37F8E1B2684B3905 CRC64;	
SQ		
Query Match	44.7%; Score 1110; DB 4; Length 311;	
Best Local Similarity	66.6%; Pred. No. 1.9e-75;	
Matches 203; Conservative	51; Mismatches 51; Indels 0; Gaps 0.	
QY	173 DIGDSLITPDETFDEKKSQWMMROLLAGLIGAVSRSTAPDLRLKIMQVHGSKDKM	232
Db	7 DVGEMULIPDETTEYEROTGMMWRILVAGGAGAVSRCTAPDLRLKIMQVHGSKDKM	66
QY	233 NIFGGFROWMKBGKTRSLMRNGTGNVIRIAPETAVFMAVEQYKRLLEEGOKIGTFERF	292
Db	67 GIVGGFROWMKBGKTRSLMRNGTGNVIRIAPETAVFMAVEQYKRLLEEGOKIGTFERF	126
QY	293 ISGSMAGTACTFTIPEMEVMTKRLAVGKTGQSGIYDCAKRLILKEGGAFAFGKGYVPMIL	352
Db	127 VAGSLAGAIQAOSIIPMEVLKTRMAIRRTGTQSGIMLDCARRILAEAGVAAFYKGYVPMIL	186
QY	353 GIIPYAGIDILAYEELKSWIDNFKDSVNPVPMILGALISSTGGGLASTPLALVTRT	412
Db	187 GIIPYAGIDILAYEELKSWIDNFKDSVNPVPMILGALISSTGGGLASTPLALVTRT	246
QY	413 MQAQMAGSPDLNNGVGFERRILISKEGIPGLRGITTPNFKVLPAVAGISVYVYENKQTL	472
Db	247 MQAQMAGSPDLNNGVGFERRILISKEGIPGLRGITTPNFKVLPAVAGISVYVYENKQTL	306
QY	473 GYTOR 477	
Db	307 GYTOR 311	
RESULT	8	
99VITX3		

ID 09VWX3 PRELIMINARY; PRT; 370 AA.  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-Oct-2001 (TReMBLrel. 18, Last annotation update)  
 DE CG4392 PROTEIN.  
 GN CG4392.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_taxid=7227;  
 RP [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY.  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mottman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Branton R.C., Rogers Y.-H.C., Blaziel R.G., Chame M., Pfeiffer B.D.,  
 RA Man K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Plankh C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cayley S., Dahlke C., Davenport L.B., Davies P.,  
 RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Flosser C., Gabriellian A.E., Gaig N.S., Gelbart W.M., Glasser K.,  
 RA Glöckner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,  
 RA Jajani M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinelt K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spraker E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirsky R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang M., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL  
 CC INNER MEMBRANE (BY SIMILARITY)  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 CC EMBL: AEO03541; AAF49922.1; -;  
 CC FLYBase: FBgn0036283; CG4392.  
 DR InterPro: IPR001993; Mitoch.carrier.  
 DR InterPro: IPR002067; Mit.carrier.  
 DR Pfam: PF00153; mito.carri: 3.  
 DR PRINTS: PR00926; MITOCARRIER  
 DR PROSITE, PS00215; MITOCH\_CARRIER: 1.  
 RW Inner membrane; Mitochondrion; Transmembrane; Transport.  
 SW SEQUENCE 370 AA: 41539 MW: 944F1BA9A5E5CCE1 CRC64:

Query Match	36.4%	Score 902;	DB 5;	Length 370;
Best Local Similarity	53.4%;	Pred. No. 1,1e-59;		
Matches 182;	Conservative 56;	Mismatches 75;	Indels 26;	Gaps

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Db      : 28 MEDVIVIFDMNGRLLDIDGEDMNVADDDTQKEMQTGLMKRWLLVAGGILAGAVSRKTCTPLD    87
Oy      : 217 RUKIMMYHGSK-----SDKMIEGGFRQWYVEGGIRSLMRONGTNVIKIAPETAVKFMAY    277
Db      : 88 RIKVYLQWNPRTVOTOTOMGISICECHMLINDBGSSRMWRNGINVLKIAPETAFKFAAY    147
Oy      : 273 EGYKKLL--TEEGOKITGIFERFISSMAGATAQFTIYYMEVPMKTRLANGTKGOYSGIYC    330
Db      : 148 EGMKRLIRDDDSRRMSIVEREYFAGAAGGISQTIITYPEVLEKTRLARTRTGQYGIADA    207
Oy      : 331 AKKIKLHEGIGAFYKGYPENLLGITPYAGIDLAVELLSYWLNDNFAKDSVPNPMVLLG    390
Db      : 208 AKYIKTGEBVRSEFYGVYNNILIGILIPYAGIDLAVETLKRYTIANH-DNNQPSFIVLLA    266
Oy      : 391 CGALSTTCGQLASYPDLAVTRTRMQAQM-----LEGSP-----QLNNVGLERR    433
Db      : 267 CCGSTSTLGQLCSTYPLAVLTRFLQAQAAETTANOKRKQIPLKSSDAHSGETWTGFLFK    326
Oy      : 434 IISKEGIBGLYRGITPNPMKYLPANGISVYVENMKQTLGV    474
Db      : 327 IVRSBGLTYRGITPNEKLVAHSVSYVVEYTSRALGI    367

RESULT          9
OyFI43
ID      : 09FI43. PRELIMINARY; PRT; 487 AA.
AC      : 09FI43.
DT      : 01-MAR-2001 (TREMBLrel. 16, Created)
DT      : 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE      : 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
OS      : CALCIDIUM-BINDING TRANSPORTER-LIKE PROTEIN.
OC      : Arabidopsis thaliana (mouse-ear cress).
OC      : Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC      : Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: rosidae:
OC      : eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX      : NCBI_TaxID=3702; [1]
RN      :
RC      : SEQUENCE FROM N.A.
RP      : STRAIN-COLUMBIA;
RX      : MEDLINE=99397451; PubMed=10470850;
RA      : Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
RA      : Miyajima N., Tabata S.:
RT      : "Structural analysis of Arabidopsis l-thal1,550 bp covered by seventeen
RT      : pl and TAC clones."
RL      : DNA Res. 6:183-195(1999).
DR      : EMBL, AB017063; BAB08751.1; -
DR      : HSBP; P09860; IFS.
DR      : InterPro; IPR002048; EF-hand.
DR      : InterPro; IPR001993; Mitoch_carrier.
DR      : Pfam; PF00153; mito_carr_3.
DR      : PRINTS; PR00926; MITOCARRIER.
DR      : SMART; SM0054; EFh_2.
SQ      : PROSITE; PS00018; EF_HAND; UNKNOWN_1.
SQ      : SEQUENCE 487 AA; 54505 MW; 22688650C0841537 CRC64;
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Query Match Similarity      35.7%: Score 885.5; DB 10; Length 487;
Best Local Similarity      40.6%: Pred. No. 2,9e-58;
Matches 190; Conservative  89; Mismatches 156; Indels 33; Gaps 9

QY  19 EGPRTRETLQALDRNGDGVVDIGELQGLRNIGIPLGQDAEIKFTTGDVYKDKGLDFE 78
    | : | : | | : | : | : | : | : | : | : | : | : | : | : | : |
Db  36 EKDILIRSFSPFSDSENNVGYLDCAOIEKGLCALQIPSGYKAKELFRVCDANRDRGVYD 95
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY  79 ERMKTLKDEHKMKMLAFKSLDKNNNGKTIASGLVSLQTLGTLTSEQQALSLGSDVDVG 138
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  96 EERRIVADKDELFLYRFQALIDVHNKCSISPEGLMDSLVKAGIETIDDELARVEVHDKDN 155
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 139 TMTVDMNMRDQYFLNP-VTDIEETIRFKMHSGTGIDGSLTIPDETFEDEKSKQWNR 197
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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Db 156 DGIIMEFWRDELLLYPHEATTENITYHHMERVCLVDIGQAVIPGDISKHRSNYF--- 212
Oy 198 LLAGIAGAVSRSTAPDLRLKIMQVHGSKSDKMNIFGCFROMYKEGIRSLMRNGNTN 257
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 213 -IAGGIAGAASTATAPDLRLKVLQI--QKTD-ARIRAIKILIKOGSVRFRRNGIN 268
Oy 258 VIKIAPETAVKFWAYEQYKRL---LTEBQKIGTFEERFISGSMAGATQTFIYMEVVK 313
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 269 IYKVAPESAIKFEYAELEFNAIGENMGEDKADIGTIVRLFAGMGAGAVQASITPLDIYK 328
Oy 314 TRL-----AVGKTGYSGIYDCAKKILKHEGICAFYKGYVNLGIIYAGIDLAV 364
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 329 TRLQYTSQAGVAPRLGLT-----KDLVHEGPRAYKGLFPLSLGIIYAGIDLA 382
Oy 365 YELLKSYWLDNFAKDSVNGVWVLLGCGALSTCGOLASYPALVYTRMQAQMLEGSPQ 424
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 383 YETLNDLSTYIILQDA-EGGPLVQJGCGTISGALATCYPIQVYRTRMQAE-----RAR 436
Oy 425 LNMVGLFRRITSEKIGIPGLYRGTPEMKVLPVAGISYVYENMKOTL 472
Db 437 TSMGVSFRRITSEEGYRALYKGLPLNLKVPAPASITYVYEAAMKSL 484

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RESULT 10
O9LY28 PRELIMINARY; PRT; 479 AA.
AC O9LY28;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PEROXISOMAL CA-DEPENDENT SOLUTE CARRIER-LIKE PROTEIN.
GN T211_30.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AL163912; CAB87921.1; -.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001986; EFP_synthase.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00104; EFP_SYNTHASE_1; UNKNOWN_2.
DR PROSITE; PS00215; MITOCH_CARRIER_1; UNKNOWN_1.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 479 AA; 53969 MW; 38D58E1395316D6E CRC64;

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Query Match 34.3%; Score 852; DB 10; Length 479;
Best Local Similarity 39.4%; Pred. No. 9.3e-56;
Matches 181; Conservative 90; Mismatches 172; Indels 16; Gaps 6;
Oy 19 EOPRYETLFOALDRNGGVVDIGELQELRLNLGIPLGQDAEKKITFTGVNKKDKLDFE 78
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 33 EREIRISLDFPDNSNLGFLDYAQIEKGLASLQIPPEYKVARDLFRVCADNRGRVDYQ 92
Oy 79 EFMKLRKHKKMKLAFLKSLKNNKGKIFASIVSLOTILGTLISEQQAELLISIDVDG 138

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Db 93 EFRRYIDAKELLYRIFQADIVENHNCCLLPETLMALVYAGIEIDDEELARVEVHDXDN 152
Oy 139 TMTVMNENRQYELFNP-VTDIEEIRFPWKHSTGIDIGSLTIPPEFDEKSGQMMRQ 197
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 153 NCTTFEERWDFLLYPHEATTENITYHHMERVCLVDIGQAVIPGDISKHRS-----RL 208
Oy 198 LLAGIAGAVSRSTAPDLRLKIMQVHGSKSDKMNIFGCFROMYKEGIRSLMRNGNTN 257
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 209 LLAGIAGAVSRSTAPDLRLKVLQVQRAHA---GVLPYIKIRWEDKLMGFRRNGIN 265
Oy 258 VIKIAPETAVKFWAYEQYKRLKLTBEGQKIGTFEERFISGSMAGATQTFIYMEVVKRL- 316
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 266 VIKVAPESAIKFEYAELEFNAIGENMGEDGDTGSGRLMAGMAALQATALYPMDLVYKRLQ 325
Oy 317 -AVGKTGYSGIYDCAKKILKHEGICAFYKGYVNLGIIYAGIDLAVYELLKSYWLDN 375
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 326 TCYSEGRKAPKMKLTKDLVWEGPRAYKGLFPLSLGIIYAGIDLAAYELTKDLSTRY 385
Oy 376 FAKDSVNGVWVLLGCGALSTCGOLASYPALVYTRMQAQMLEGSPQLNNGVLFRRIL 435
Db 386 ILQDT-EGGPLVQJGCGTISGALASCVYPIQVYRTRMQAD-----SSKTKKQEFMNTM 439
Oy 436 SKEGIPGLYRGTPEMKVLPVAGISYVYENMKOTLGY 474
Db 440 KEGGLRGFYRGLPLNLKVPAPASITYVYEAAMKSL 478

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RESULT 11
O9FLS8 PRELIMINARY; PRT; 478 AA.
AC O9FLS8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PEROXISOMAL CA-DEPENDENT SOLUTE CARRIER-LIKE PROTEIN (PUTATIVE
DE PEROXISOMAL CA-DEPENDENT SOLUTE CARRIER PROTEIN).
GN MAC9_13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98290546; PubMed=9628582;
RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
RT Sequence features of the regions of 1,456,315 bp covered by nineteen
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:41-54(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,
RA Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
RA Kosegawa E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shim P.,
RA Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene MAC9_13 (GI:10176874).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010069; BAB10081.1; -.
DR EMBL; AY056219; AAL07068.1; -.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR SMART; SM00054; EFh; 4.

```







DB 274 MCGWKDASAIYTCGSGRSTASLEXYTGWADAFKATVRHGFALYKGLVPNVKVPSTIAIA 333  
OY 462 YVYVENMKOTLGV 474  
DB 334 FVYVENKDVLG 346

Search completed: August 18, 2002, 09:30:28  
Job time: 483 sec

## RESULT 15

O9FU82 PRELIMINARY; PRT; 322 AA.  
AC O9FU82;  
DT 01-MAR-2001 (TREMBLrel, 16, Created)  
DT 01-MAR-2001 (TREMBLrel, 16, last sequence update)  
DT 01-JUN-2001 (TREMBLrel, 17, last annotation update)  
DE PUTATIVE PEROXISOMAL CA-DEPENDENT SOLUTE CARRIER PROTEIN.  
GN P0019D06.21 OR P0024G09.9.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV, NIPPONBARE;  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC  
clone:P0019D06.";  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV, NIPPONBARE;  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC  
clone:P0024G09.";  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP002483; BAB16462.1; -;  
DR EMBL; AP003311; BAB40117.1; -;  
DR InterPro: IPR001993; Mitoch\_carrier.  
DR InterPro: IPR002067; Mit\_carrier.  
DR InterPro: IPR002030; Mit\_uncoupling.  
DR Pfam; PF00153; mito\_carr; 3.  
DR PRINTS; PR00926; MITOCARRIER.  
DR PRINTS; PR00784; MTUNCOUPLING.  
DR PROSITE; PS00215; MITOCH\_CARRIER; UNKNOWN\_1.  
SQ SEQUENCE 322 AA; 34876 MW; A649A692FBA6BD69 CRC64;

Query Match 21.0%; Score 520; DB 10; Length 322;  
Best Local Similarity 40.5%; Pred. No. 4.7e-31;  
Matches 117; Conservative 51; Mismatches 103; Indels 18; Gaps 7;

OY 198 LLAGGTAGAVSRSTAPDLRLKIMOVHGKSP-----KMNFGFRQWYKEGINSLSR 252  
DB 29 LAAGGFGAGAVSKTCTAPLRLTLTFQVAGHSDVAALKKYSIMHEASRIYREGFGAFWK 88  
OY 253 GNGTNYIKIAPFAVKKEMAYEOKKL-----LTREGQKIGTFERFISGSMAGATAQTFI 306  
DB 89 GNLVTIVHRLPYSAISFYSTERYKKFLQRYVPGIDEDSNVYGV-ARLLSGGLAGTTASVT 147  
OY 307 YPMENKKTRLAVGTQ-QYSGIYDCAKKILKHGLGAFYKGVVYNLGIIPYAGIDLAVY 365  
DB 148 YPLDVVTRTLAQTKTRYYKGIHNAVSTICRDEGVKGLYGLGATLLGVGPSIAISFTVY 207  
OY 366 ELLKSTWLDNFADSVNPGVMVLLGGGALSSTGQLASTYPLALVTRTRMQAAMLEGSP-- 423  
DB 208 ESLRSHQMERPDQS--PAVVSLSFS-GSLSGIASSTATFPLDLVKRRMQLQGAAGTSVVC 264  
OY 424 QLNWVGLEFRIISKEGIPGLYRGITPNEMKLEPAVGISYVYVENMKOTL 472  
DB 265 KSSITGTIRQIFQKEGIRGFTYRGIVPEYIKVPSVGIATFMTETLSL 313







QY	1561	cccgaaatgatgtgtcattttttgctttaagccgtgaatgaaacttcaaacactct	1620
Db	1561	cccgaaatgatgtgtcattttttgctttaagccgtgaatgaaacttcaaacactct	1620
QY	1621	ggaatgacttttctccctgaatttgaaacaaagctctatgcaaaagaatctcatcttt	1680
Db	1621	ggaatgacttttctccctgaatttgaaacaaagctctatgcaaaagaatctcatcttt	1680
QY	1661	cacaaagggaagacggtaaacaaatggtacattcaacttttggcttaatatatgtaca	1740
Db	1661	cacaaagggaagacggtaaacaaatggtacattcaacttttggcttaatatatgtaca	1740
QY	1741	cagaatagttccaatatcatatgatttttaatgtgttttggaaaaggccacacatatactta	1800
Db	1741	cagaatagttccaatatcatatgatttttaatgtgttttggaaaaggccacacatatactta	1800
QY	1801	tctttcttaataatccctgcgaatccctcctgcctgtaaccggaatctgaaaatgtacgtgc	1860
Db	1801	tctttcttaataatccctgcgaatccctcctgcctgtaaccggaatctgaaaatgtacgtgc	1860
QY	1861	ttgaaacaaatgtgtttgt	1920
Db	1861	ttgaaacaaatgtgtttgt	1920
QY	1921	ttaagtttaagcagatctcccttaattataattctctgtttatatatttgaatgtct	1980
Db	1921	ttaagtttaagcagatctcccttaattataattctctgtttatatatttgaatgtct	1980
QY	1981	tatagattcttctaataattccttatagaacccattatagaataatcattatcaattaaata	2040
Db	1981	tatagattcttctaataattccttatagaacccattatagaataatcattatcaattaaata	2040
QY	2041	taccttaacgcaaaagatcccaataatagataggtttatgtccctattttcttcagc	2100
Db	2041	taccttaacgcaaaagatcccaataatagataggtttatgtccctattttcttcagc	2100
QY	2101	tgaatacgaatgtaacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc	2160
Db	2101	tgaatacgaatgtaacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc	2160
QY	2161	tcaatgagcactttccatttaccacacgttaccattatttggcttccgtgtatacaact	2220
Db	2161	tcaatgagcactttccatttaccacacgttaccattatttggcttccgtgtatacaact	2220
QY	2221	aatttcagatatactctgttaataattaccacaacagaagaattttgaaagcttcgt	2280
Db	2221	aatttcagatatactctgttaataattaccacaacagaagaattttgaaagcttcgt	2280
QY	2281	ttaactgcacatgtcttggaaaagcagcagcagcagcagcagcagcagcagcagcagc	2340
Db	2281	ttaactgcacatgtcttggaaaagcagcagcagcagcagcagcagcagcagcagcagc	2340
QY	2341	ctgagaagcactttgttcccttggcttccctgttccctacatttggataagattccgt	2400
Db	2341	ctgagaagcactttgttcccttggcttccctgttccctacatttggataagattccgt	2400
QY	2401	tttagtcaagaagaactcttctggagacacattctagtaactcgtgaatattcttttaattgc	2460
Db	2401	tttagtcaagaagaactcttctggagacacattctagtaactcgtgaatattcttttaattgc	2460
QY	2461	atgaagatgatatcatcatgaagaatgtagtggccttatttccctcaactgtgaatatac	2520
Db	2461	atgaagatgatatcatcatgaagaatgtagtggccttatttccctcaactgtgaatatac	2520
QY	2521	cttgaactctgccttctgcaatactggcagcagcacaagaagggaagagatgcctataatc	2580
Db	2521	cttgaactctgccttctgcaatactggcagcagcacaagaagggaagagatgcctataatc	2580
QY	2581	ggcgggagtgatgacttctgaaaacatltgtaaccctatttggaaaagggaaggcccaa	2640
Db	2581	ggcgggagtgatgacttctgaaaacatltgtaaccctatttggaaaagggaaggcccaa	2640

QY	2641	ttttgggaaacatataccatgcgatgtcttcg	2673
Dd	2641	tttggggaaacatataccatgcgatgtcttcg	2673
RESULT 2			
US-09-522-303-1193			
; Sequence 1193, Application US/09522303			
; GENERAL INFORMATION:			
; APPLICANT: Gearing, David P.			
; APPLICANT: Holzman, Douglas A.			
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A			
; TITLE OF INVENTION: HUMAN MAMMARY EPITHELIAL LIBRARY			
; FILE REFERENCE: 1600.1086-.001			
; CURRENT APPLICATION NUMBER: US/09/522,.303			
; CURRENT FILING DATE: 2000-03-08			
; EARLIER APPLICATION NUMBER: 60/123,393			
; EARLIER FILING DATE: 1999-03-08			
; NUMBER OF SEQ ID NOS: 1353			
; SOFTWARE: FASTSEQ for Windows Version 3.0			
; SEQ ID NO 1193			
; LENGTH: 3537			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-522-303-1193			
Query Match            94.2%;    Score 2519;   DB 19;   Length 3537;			
Best Local Similarity   99.3%;   Pred. No. 0;			
Matches 2550;   Conservative   0;   Mismatches   15;   Indels   2;   Gaps   2.			
QY	1	ccgcaaccccagcagcgcccccaaacgcttgttcgccgcgcgcccccagccagccgcgc	60
Dd	38	ccgcaaccccagcagcgcccccaaacgcttgttcgccgcgcgcccccagccagccgcgc	97
QY	61	gcgcctgctccgcgtctcgccccgcagccctcgatctccgtgactctctgcgcaggcgc	120
Dd	98	gcgcctgctccgcgtctcgccccgcagccctcgatctccgtgactctctgcgcaggcgc	157
QY	121	cctgcgcctcttgagcccatgtgcgctgtgctgcggagacttcgcctgcgccaccgcgcgc	180
Dd	158	cctgcgcctcttgagcccatgtgcgctgtgctgcggagacttcgcctgcgccaccgcgcgc	217
QY	181	gccagaagcgcgagagcagccgcagcgccttaagagaccctctccaagcaactgcagccaatg	240
Dd	218	gccagaagcgcgagagcagccgcagcgccttaagagaccctctccaagcaactgcagccaatg	277
QY	241	gggaagcagatggcttgacacatcgcgagcgtlcaaggagggtcacaagaccttgcacatccctc	300
Dd	278	gggaagcagatggcttgacacatcgcgagcgtlcaaggagggtcacaagaccttgcacatccctc	337
QY	301	tgggcgcagagcgcgcagagagaataattttactactctggagagtccaacaagatgggaagc	360
Dd	338	tgggcgcagagcgcgcagagagaataattttactactctggagagtccaacaagatgggaagc	397
QY	361	tggattttgaagaatttatgaagtagccttaagaccatagaagaagaataagaattggcatt	420
Dd	398	tggattttgaagaatttatgaagtagccttaagaccatagaagaagaataagaattggcatt	457
QY	421	ttaagaagtttaagacaanaataatgaatggaaaatttgagcttcagaanaattgtccagcttc	480
Dd	458	ttaagaagtttaagacaanaataatgaatggaaaatttgagcttcagaanaattgtccagcttc	517
QY	481	tccagacacatggctgtgactattcttgaacaacaagcagagttgatctcttcaagaacatg	540
Dd	518	tccagacacatggctgtgactattcttgaacaacaagcagagttgatctcttcaagaacatg	577
QY	541	atgttgatggggcaatlgaacatgacgtggacttgaatgaatlgagagaaacttctaattaac	600
Dd	578	atgttgatggggcaatlgaacatgacgtggacttgaatgaatlgagagaaacttctaattaac	637
QY	601	ctgttacagacacttgaagaattatcacgtllcttgaagaacattctacaggaatttgacatg	660

Db 638 ctgttaacagacaltgaggaaattatccgtttcttggaacaattacaggaattgacatag 697  
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Db 698 gggatagcttaactatccagatgaattcaacggaagacgaaaaaaatccggacaatggt 727  
Qy 721 ggaagcagcttttggcagagagcattgctggtgctctctcgacaagaactgcccct 760  
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Db 938 gtacaaacgtcatcaaatatgctcctcgagacagctgttaaatctgaggcatatgaacagt 997  
Qy 961 acagaagttactacttgagaagaagacaaaataaggacatttgagagattattcttg 1020  
Db 998 acagaagttactacttgagaagaagacaaaataaggacatttgagagattattcttg 1057  
Qy 1021 gtccatctggtgagcaactgacacagacttlaatalaccatgtaggtatgtaaaacca 1080  
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Qy 1861 ttgaacaaaattgtgttggtgttagaggtataaataatcattacttctcggtgtgc 1920  
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Qy 1921 ttacgtttatgccaagttcccttataatttaaatctctgttttataatttgaatgctt 1980  
Db 1958 ttacgtttatgccaagttcccttataatttaaatctctgttttataatttgaatgctt 2017  
Qy 1981 tatagattcctttaaatctccttatatgaacacataatagaanaatcatattataaata 2040  
Db 2018 tatagattcctttaaatctccttatatgaacacataatagaanaatcatattataaata 2077  
Qy 2041 taacttaacgcaaaagcatcccaataatagtaaggtttatgtccttatatttcttcagc 2100  
Db 2078 taacttaacgcaaaagcatcccaataatagtaaggtttatgtccttatatttcttcagc 2137  
Qy 2101 tgaatacgaatgaaacagctgtgtgaattctgaaagggaagtgaatgaattatatt 2160  
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Qy 2161 tcaagtggcaactttccatttccacacgtgacacattatgttctcgtgagttatcac 2220  
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Qy 2221 aatttcagtatatactctgttaataatcacacaacaggaacatttatgaaagattccgt 2280  
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Db 2498 atgaagtgtatgtatcatgaagcagatgtatgtcttattcttccctcactgtgtaatac 2555  
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RESULT 3  
US-09-649-163-8441  
; Sequence 8441, Application US/09649163  
; GENERAL INFORMATION:  
; APPLICANT: Holtzman, Douglas A.  
; APPLICANT: Galvin, Katherine A.  
; APPLICANT: Leiby, Kevin R.  
; APPLICANT: Kingsbury, Gillian A.  
; APPLICANT: Weich, Madeline S.  
; APPLICANT: McCarthy, Sean A.  
; APPLICANT: Williamson, Mark  
; APPLICANT: Richardson, Jennifer  
; APPLICANT: Macbeth, Kyle J.  
; APPLICANT: Fraser, Christopher C.  
; APPLICANT: Villeva, Jean-Luc M.G.





Db	1786	caggaatggttccaataatcavatgatgttttaatigtgtttggaaggccacacaaattataacttta	1845
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Db	1846	tctttcttaataaactccgtgcaaacctctgcgcctgaaatccgaaatctgaaatgtracgtgc	1905
Qy	1861	ttgacaacaaattgtttgtgtgtttgagtttaataactaaactaaacttaactttatctgggtgt	1920
Db	1906	ttgacaacaaattgtttgtgtgtttgagtttaataactaaactaaacttaactttatctgggtgt	1965
Qy	1921	ttacgtttatgcagttctccttaataatttaattcctgtgtttataatattgnaatgctct	1980
Db	1966	ttacgtttatgcagttctccttaataatttaattcctgtgtttataatattgnaatgctct	2025
Qy	1981	tatagattttctttaaatttctcttaataagaaacattataagaaaatcaatgaactttaaata	2040
Db	2026	tatagattttctttaaatttctcttaataagaaacattataagaaaatcaatgaactttaaata	2085
Qy	2041	taccttaacgacaaagatccaaatcaataagatagaggttttatgcaccttaatttcttcagc	2100
Db	2086	taccttaacgacaaagatccaaatcaataagatagaggttttatgcaccttaatttcttcagc	2145
Qy	2101	tgaatacgaatgaacacacagtggtgtggaatttctgaaagggaatgtagaattatattatt	2160
Db	2146	tgaatacgaatgaacacacagtggtgtggaatttctgaaagggaatgtagaattatattatt	2205
Qy	2161	tcaatgagcactttccattcaatttcaacacttacatatttgtttccgtgagtttaacact	2220
Db	2206	tcaatgagcactttccattcaatttcaacacttacatatttgtttccgtgagtttaacact	2265
Qy	2221	aatttcagatataactagttaataattcaacaacaaagcaatttatgnaagaattccgt	2280
Db	2266	aatttcagatataactagttaataattcaacaacaaagcaatttatgnaagaattccgt	2325
Qy	2281	ttatccgcgcattgctttgnaaaggcagggaaagaaattttgactgtatcagct	2340
Db	2326	ttatccgcgcattgctttgnaaaggcagggaaagaaattttgactgtatcagct	2385
Qy	2341	ctcgagaagcactcttgtttcttccttgccttgtttccaccctttgtaagaattccgt	2400
Db	2386	ctcgagaagcactcttgtttcttccttgccttgtttccaccctttgtaagaattccgt	2445
Qy	2401	tttagtcaagaaagactcttctgggacacattcttaagtaactgtaattctttttaatgtc	2460
Db	2446	tttagtcaagaaagactcttctgggacacattcttaagtaactgtaattctttttaatgtc	2505
Qy	2461	atgaagtcggaattacatgacgacgaatgagtggtcttatcttcctccactgtagtaatc	2520
Db	2506	atgaagtcggaattacatgacgacgaatgagtggtc-ttatcttcctccactgtagtaatc-	2563
Qy	2521	ctttgaactgcgtgttgcataatgagcgacgacacaaaggggagagata	2567
Db	2564	ctttgaactgcgtgttgcataatgagcgacgacacaaaggggagagata	2610
RESULT 4			
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: Sequence 6793, Application US/09652121			
: GENERAL INFORMATION:			
: APPLICANT: Distefano, Peter			
: TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES			
: TITLE OF INVENTION: THEREOR			
: FILE REFERENCE: 1600.1188-001			
: CURRENT APPLICATION NUMBER: US/09/652,121			
: CURRENT FILING DATE: 2000-08-30			
: PRIOR APPLICATION NUMBER: 60/151,129			
: PRIOR FILING DATE: 1999-08-30			
: NUMBER OF SEQ. ID NOS: 7615			
: SOFTWARE: FastSeq for Windows Version 4.0			
: SEQ ID NO 6793			
: LENGTH: 3545			
: TYPE: DNA			
: ORGANISM: Homo sapiens			

US-09-652-121-6793									
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DB	46	ccggaaccccggaacggcgcccccacaaacgctcttttggccgagcgcccgcccgacgcccgcctc	105						
QY	61	gcgcctgtcccggtctcgcgcccgacgacctcgatctcccgtagacttcctcgccagcgcg	120						
DB	106	gcgctgtcccggtctcgcgcccgacgacctcgatctcccgtagacttcctcgccagcgcg	165						
QY	121	ccctgcgaccttggagacatgtttgcctgtgctcgcgagacttcgctgtgccacccggygct	180						
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QY	181	gccagagacgagagacagccagcgctatagagaccccttcacagacatggagccgaatg	240						
DB	226	gccagagacgagagacagccagcgctatagagaccccttcacagacatggagccgaatg	285						
QY	241	ggagcggagtggttggacatctgcgcgagctcgcagagaggggctcagagaaactggatccctc	300						
DB	286	ggagcggagtggttggacatctgcgcgagctcgcagagaggggctcagagaaactggatccctc	345						
QY	301	tgggcccagggcgccggagggagaaattttactacttgagagtctcaacaaagtggagaagc	360						
DB	346	tgggcccagggcgccggagggagaaattttactacttgagagtctcaacaaagtggagaagc	405						
QY	361	tggatttttggagaatttatbtaagtaaccttaagacccatagagagaaatgtgaattggcat	420						
DB	406	tggatttttggagaatttatbtaagtaaccttaagacccatagagagaaatgtgaattggcat	465						
QY	421	ttaaagatttagacacaaataataatgataggagaaatttgaagcttcacgaattgtccagttcc	480						
DB	466	ttaaagatttagacacaaataataatgataggagaaatttgaagcttcacgaattgtccagttcc	525						
QY	481	tccagacacctgggctctcaactattctcgaaacaaagcaagtttgattctctcaagcatg	540						
DB	526	tccagacacctgggctctcaactattctcgaaacaaagcaagtttgattctctcaagcatg	585						
QY	541	atgtttgatgggacaaatgacgvtggacttggatagaaatgtgagagactacttctattaatc	600						
DB	586	atgtttgatgggacaaatgacgvtggacttggatagaaatgtgagagactacttctattaatc	645						
QY	601	ctgttgaagacattggaggaattatccggtttctcgagaaactctacaggaatttgcacag	660						
DB	646	ctgttgaagacattggaggaattatccggtttctcgagaaactctacaggaatttgcacag	705						
QY	661	gggagtaagcttaactacttcagatgtaattcagcaggaagcagaaaaaactccgagcaatggt	720						
DB	706	gggagtaagcttaactacttcagatgtaattcagcaggaagcagaaaaaactccgagcaatggt	765						
QY	721	ggagagcagccttttggcagggagggcattgtcgcgtggtctcttggaaacagccctgcctt	780						
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QY	781	tggagcccttcggaataatcatbatagtcaggtttcacaggtttcaaaaatccagacaaatgaaacat	840						
DB	826	tggagcccttcggaataatcatbatagtcaggtttcacaggtttcaaaaatccagacaaatgaaacat	885						
QY	841	ttgtgtgcttctcgacagatgtgtaaaagagagagtaaccgctgcgcttttggaggggaatg	900						
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QY	901	gtacaaaacgtcatcaaaaattgtcctccgagagacgctttaaattcttgggcataatggaacgt	960						
DB	946	gtacaaaacgtcatcaaaaattgtcctccgagagacgctttaaattcttgggcataatggaacgt	1005						
QY	961	acaagaagttactbacttgagagagagacaaataatgaaacatttggagattatttttg	1020						

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Dh 1966 ttaagttatgacagctcccttatatttaattctgtttatataatttgaatgtctt 2025
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Dh 2026 tatagattctttaaatcttccctta tagaacaatlaagaaatcatcatatcttaaaata 2085
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Dh 2506 atgaagttgattgatcatcagagcagaagtgtatggccttatttccctcactgtgtatc 2563
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RESULT 5
US-09-652-123-9069
; Sequence 9069, Application US/09652123
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NOCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1186-001
; CURRENT APPLICATION NUMBER: US/09/652,123
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,135
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 9796
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9069
; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-123-9069
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Best Local Similarity 99.3%; Pred. No. 0; Mismatches 16; Indels 2; Gaps 2;
Matches 2549; Conservative 0;
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Qy 61 ggcgtgttcccggttctgcgcccgacgcctcgatctccgtgtacttctctggcagcg 120
Dh 106 ggcgtgttcccggttctgcgcccgacgcctcgatctccgtgtacttctctggcagcg 165
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[illegible]

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QY	1381	ctcaagcattttagaaggtctcccaacagctaaatctgttggcctcttgcagaata	1440
Dp	1426	ctcaagcattttagaaggtctcccaacagctaaatctgttggcctcttgcagaata	1485
QY	1441	ttcccaagaagaataccaggaactttagaagcaltcaccccaactctabgaagctgc	1500
Dp	1486	ttcccaagaagaataccaggaactttagaagcaltcaccccaactctabgaagctgc	1545
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Dp	1666	ggagtgaccttttctcctcgaaatgaaacagctatgacaaagaagctgcattttt	1725
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Dp	1786	cagaatgttcaaatcatagttttaaagtgtttgaaaggccacaaatataactta	1845
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Dp	1846	tcttttcttaatactctgcgaactctgcgcctgtaaccgaaactctgaaatgtactgc	1905
QY	1861	ttgaaacaaatgtgtttgtgttagagtttaaatactataactttatctgggtgt	1920
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Dp	1966	ttaagttatgcgcgttcccttataatattctgtttatataattttagatgtct	2025
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Dp	2026	tatagatttctttaaatttcccttatagaaaccttaataagaaatcatatcataata	2085
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QY	2341	ctgcaagacatcttgttttctccttgccttgccttgcctacactttgaaatcagattcgt	2400
Dp	2386	ctgcaagacatcttgttttctccttgccttgccttgcctacactttgaaatcagattcgt	2445

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; Sequence 8162, Application US/096552918  
; GENERAL INFORMATION:  
; APPLICANT: Galvin, Katherine  
; APPLICANT: Holtzman, Douglas A.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 1600.1187-001  
; CURRENT APPLICATION NUMBER: US/09/652,918  
; CURRENT FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/151,130  
; PRIOR FILING DATE: 1999-08-30  
; NUMBER OF SEQ ID NOS: 8985  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8162  
; LENGTH: 3545  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-652-918-8162

Query Match 94.2%; Score 2517.4; DB 25; Length 3545;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 2549; Conservative 0; Mismatches 16; Indels 2; Gaps 2;

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QY 61 ggcgtgtcccggtctgc 120  
Db 106 ggcgtgtcccggtctgc 165  
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QY 241 gggagcagatgtgtgacatcgcgagctgcgagggggggtcgaagaaacttggaactccctc 300  
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QY	1921	ttacggttaatgcagcttcctcttaatttcaattctctgtttataataatttgaaatgct	1980
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; GENERAL INFORMATION:			
; APPLICANT: Holtzman, Douglas A.			
; APPLICANT: Gearing, David P.			
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES			

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1  TITLE OF INVENTION: THEREFOR
2  FILE REFERENCE: 1600.1198-001
3  CURRENT APPLICATION NUMBER: US/09/667.617
4  CURRENT FILING DATE: 2000-09-21
5  PRIOR APPLICATION NUMBER: 60/155,295
6  PRIOR FILING DATE: 1999-09-21
7  NUMBER OF SEQ ID NOS: 2254
8  SOFTWARE: FastSeq for Windows Version 4.0
9  SEQ ID NO 1724
10 LENGTH: 3545
11 TYPE: DNA
12 ORGANISM: Homo sapiens
13 US-09-667-617-1724

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[illegible]



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Qy 2521 ctttgaactgtcttgcacaatctgagcagcagcagcagcagcagcagcagcagcagcagc 2567  
Dh 2564 ctttgaactgtcttgcacaatctgagcagcagcagcagcagcagcagcagcagcagcagc 2610

RESULT 8  
US-09-698-010-12652  
; Sequence 12652, Application US/09698010  
; GENERAL INFORMATION:  
; APPLICANT: Williamson, Mark  
; TITLE OF INVENTION: NOVEL NOCLEIC ACID MOLECULES AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 1600.2029-001  
; CURRENT APPLICATION NUMBER: US/09/698, 010  
; CURRENT FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: 60/162,358  
; PRIOR FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 15684  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12652  
; LENGTH: 3545  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-698-010-12652

Query Match 94.2%; Score 2517.4; DB 27; Length 3545;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 2549; Conservative 0; Mismatches 16; Indels 2; Gaps 2;  
Qy 1 ccgcaccccgagcgccccaacgctgttgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 60







Dh	1426	ctcaagccatgtctcgaaggttccccaagcttgatctggttgccctcttcgcgaat	1485
Oy	1441	ttcccaagaaggatataccaggaacttaccagagcatcccccacacttcataaggtgc	1500
Dh	1486	ttcccaagaaggatataccaggaacttaccagagcatcccccacacttcataaggtgc	1545
Oy	1501	ttccctgctgtagcatcaagtagtctgtgtttatgaataatagaaacaaacttaagatga	1560
Dh	1546	ttccctgctgtagcatcaagtagtctgtgtttatgaataatagaaacaaacttaagatga	1605
Oy	1561	cccagaatgtatgttcgaatttttgcctttagcctgaataatgaaacttccaacacct	1620
Dh	1606	cccagaatgtatgttcgaatttttgcctttagcctgaataatgaaacttccaacacct	1665
Oy	1621	ggatgacttttctcctcgaaattgaaacaagtcataggcaagaagctgcatttttt	1680
Dh	1666	ggatgacttttctcctcgaaattgaaacaagtcataggcaagaagctgcatttttt	1725
Oy	1681	cacaaagggaagccggttaacatggtgcatacttaaaacttttggcctaaataatggtca	1740
Dh	1726	cacaaagggaagctgtgtaacatggtgcatacttaaaacttttggcctaaataatggtca	1785
Oy	1741	cagaatgttcaaaaataagatctttaaagtgtttgaaaaggccacacataacttia	1800
Dh	1786	cagaatgttcaaaaataagatctttaaagtgtttgaaaaggccacacataacttia	1845
Oy	1801	tcctttccttaataccttgnaaactctgcgcctggaatccgaaatttgnaaatgtagtgc	1860
Dh	1846	tcctttccttaataccttgnaaactctgcgcctggaatccgaaatccgaaatgtagtgc	1905
Oy	1861	ttgaaacaaatctgtctgtgtgttagagtataaatacaatcttatttcgggtgt	1920
Dh	1906	ttgaaacaaatctgtctgtgtgttagagtataaatacaatcttatttcgggtgt	1965
Oy	1921	ttacgtttaatgcagcttccttatataattctctgttttatataatttgaatgctct	1980
Dh	1966	ttacgtttaatgcagcttccttatataattctctgttttatataatttgaatgctct	2035
Oy	1981	tatagattctcttaacttctcctataagaacatataaanaacatatactttaaata	2040
Dh	2026	tatagattctcttaacttctcctataagaacatataaanaacatatactttaaata	2085
Oy	2041	taccttaagcaaaagcatcccaataagtaaggtttatgtccttatttcttcagc	2100
Dh	2086	taccttaagcaaaagcatcccaataagtaaggtttatgtccttatttcttcagc	2145
Oy	2101	tgaatacgaatgaacacagctggttggaattcttgaagggaagtgatgaatatatttt	2160
Dh	2146	tgaatacgaatgaacacagctggttggaattcttgaagggaagtgatgaatatatttt	2205
Oy	2161	tcagtgggcacttttccatttaccacgttacatbatttgttccctggaattatacact	2220
Dh	2206	tcagtgggcacttttccatttaccacgttacatbatttgttccctggaattatacact	2265
Oy	2221	aatttcaagtatatactgtttaataatacaacaagaagaaattatttgaagaatccgt	2280
Dh	2266	aatttcaagtatatactgtttaataatacaacaagaagaaattatttgaagaatccgt	2335
Oy	2281	ttatccctgcacttgccttgaanaagcagcgaaacgaatttttgcacttgatacagct	2340
Dh	2326	ttatccctgcacttgccttgaanaagcagcgaaacgaatttttgcacttgatacagct	2385
Oy	2341	ctgcaagacatcttgcttctcctgtgcctgtgttctcctacacttgaatacagatccgt	2400
Dh	2386	ctgcaagacatcttgcttctcctgtgcctgtgttctcctacacttgaatacagatccgt	2445
Oy	2401	tttagtcaaggaagcctcttggaacatctccttagaactcgaatcttctttaatgtc	2460
Dh	2446	tttagtcaaggaagcctcttggaacatctccttagaactcgaatcttctttaatgtc	2505
Oy	2461	atgaagtgtatgttcatatggcaagtgatggtgccttattctccctcacctgtgataatc	2520

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Db      2506  atgaatgagatgatcatatgaagcaaatgagatgic-ttatttcctccatcgttgtaat- 2563
Oy      2521  cttggaactgctggttgcataataggccacaagaaggagagaga 2567
          |||||
Db      2564  cttggaactgctgttccataataggccacaagaagtgagagata 2610

RESULT 10
US-09-726-810-3387
; Sequence 3387, Application US/09726810
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600, 2016-001
; CURRENT APPLICATION NUMBER: US/09/726,810
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/160,017
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 3398
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3387
; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-726-810-3387

Query Match      94.2%; Score 2317.4; DB 29; Length 3545;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2549; Conservative 0; Mismatches 16; Indels 2; Gaps 2.

Oy      1  ccggaaccccgagcgccccaacgctgttgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 60
Db      46  ccggaaccccgagcgccccaacgctgttgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 105
Oy      61  gcgcgtgtccgcgctcgcgcccgagccctcgatctccgttactcctcgcgcgagccg 120
Db      106  gcgcgtgtccgcgctcgcgcccgagccctcgatctccgttactcctcgcgcgagccg 165
Oy      121  cctgcgcctcttgagacatgttgcgctgcgtctgcggacttcgcctcgcgccacggcgt 180
Db      166  cctgcgcctcttgagacatgttgcgctgcgtctgcggacttcgcctcgcgccacggcgt 225
Oy      181  gccagagacgcgagacgcgcgcgcgtacagagaccctctccaggcaatgcgcgcgaatg 240
Db      226  gccagagacgcgagacgcgcgcgcgtacagagaccctctccaggcaatgcgcgcgaatg 285
Oy      241  gggaacgagatggttgacatcgcgcgcgcgtcagagagggtccaggaacttggatccctc 300
Db      286  gggaacgagatggttgacatcgcgcgcgcgtcagagagggtccaggaacttggatccctc 345
Oy      301  tgggcacgaagcccgagaggaataattttactactcgagatgtccaacaagaatgggaagc 360
Db      346  tgggcacgaagcccgagaggaataattttactactcgagatgtccaacaagaatgggaagc 405
Oy      361  tggatttgaagaattatgatgaatccttaagaagccatgagaagaanaatgaaattggcat 420
Db      406  tggatttgaagaattatgatgaatccttaagaagccatgagaagaanaatgaaattggcat 465
Oy      421  ttaagaatttaacaaaaataatgatatggaanaattgaggtcttcagaanaattgcccgttc 480
Db      466  ttaagaatttaacaaaaataatgatatggaanaattgaggtcttcagaanaattgcccgttc 525
Oy      481  tccagacacttggcttcgactattcttgaaacaacaagcaagatgttgttccaaacatg 540
Db      526  tccagacacttggcttcgactattcttgaaacaacaagcaagatgttgttccaaacatg 585
Oy      541  atgttgatgaggaacaatgacagtgagcctggaatgaaatggagagagactacttataatc 600
Db      586  atgttgatgaggaacaatgacagtgagcctggaatgaaatggagagagactacttataatc 645

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QY	601	ctgttacaagaaatttgaaagaattatccggttttcvgaaacatttcaagaattgacatg	660
Db	646	ctgttacaagaaatttgaaagaattatccggttttcvgaaacatttcaagaattgacatg	705
QY	661	ggatagatttaacttccatccatgaatttcaacggaaagcgaanaaaatccggacaattgt	720
Db	706	gggataagcttaactatctccagatgaatttccagaaagcgaanaaaatccggacaattgt	765
QY	721	ggagcgacgttttvgcagaggaagcatttgcgtgtcttcttcgaanaagcactgcccctt	780
Db	766	ggagcgacgttttvgcagaggaagcatttgcgtgtcttcttcgaanaagcactgcccctt	825
QY	781	tggacccgtctgaanaatcaatgatgcaggtttcaacggttcaaaaatcagaacaatgaacata	840
Db	826	tggacccgtctgaanaatcaatgatgcaggtttcaacggttcaaaaatcagaacaatgaacata	885
QY	841	tttgggtgttttcgcaagatgttaaanaagaggtttccgctgcgttttggagggaaatg	900
Db	886	tttgggtgttttcgcaagatgttaaanaagaggtttccgctgcgttttggagggaaatg	945
QY	901	gtacaaacgttacaanaaatctgtctccttaagcagctgttaaatcttvgcatttgaacagt	960
Db	946	gtacaaacgttacaanaaatctgtctccttaagcagctgttaaatcttvgcatttgaacagt	1005
QY	961	acaagaagttacttactctgaagaagagacaaaataagaaacatttgaagattattctctg	1020
Db	1006	acaagaagttacttactctgaagaagagacaaaataagaaacatttgaagattattctctg	1065
QY	1021	gttccatggtcgtggagcaacgtgcacagcttttatatccaaatggaggttataaaccac	1080
Db	1066	gttccatggtcgtggagcaacgtgcacagcttttatatccaaatggaggttataaaccac	1125
QY	1081	ggctgcgtctgaagcaanaacgtggcagactctgtaatatatgatttgcgaagaagatt	1140
Db	1126	ggctgcgtctgaagcaanaacgtggcagactctgtaatatatgatttgcgaagaagatt	1185
QY	1141	tgaacaatgaaagctctvggagcttttacaagaagctatgttcccaatttatagttacac	1200
Db	1186	tgaacaatgaaagctctvggagcttttacaagaagctatgttcccaatttatagttacac	1245
QY	1201	tactcttgcagggatagatcttgcgtgtatgatgctcttgaagttacttatgttcgctgata	1260
Db	1246	tactcttgcagggatagatcttgcgtgtatgatgctcttgaagttacttatgttcgctgata	1305
QY	1261	attttgcaaaagatctctgttlaaacocctgaaatcttggttgcgtggagatcggttccatt	1320
Db	1306	attttgcaaaagatctctgttlaaacocctgaaatcttggttgcgtggagatcggttccatt	1365
QY	1321	ccagacacctgtgtcagcttgcgcagatcccaatttgccttvtgtgaagaaactgcacatgcag	1380
Db	1366	ccagacacctgtgtcagcttgcgcagatcccaatttgccttvtgtgaagaaactgcacatgcag	1422
QY	1381	ctcaagccatgtttagaaggtttccccaagcttgataatgttggcctcttcttgaagaata	1444
Db	1426	ctcaagccatgtttagaaggtttccccaagcttgataatgttggcctcttcttgaagaata	1485
QY	1441	tttccaagaaggaatcccgagatttacaagagcctcccccacaactcatgaagagctgc	1500
Db	1486	tttccaagaaggaatcccgagatttacaagagcctcccccacaactcatgaagagctgc	1545
QY	1501	ttccctgctgttagatcatgatattvtggttatgaanaatatgaaacaaacttttagagata	1560
Db	1546	ttccctgctgttagatcatgatattvtggttatgaanaatatgaaacaaacttttagagata	1605
QY	1561	cccgaagaatgattgtgatatttttggctttagccttgaatattgaacatttcaacaatcct	1622
Db	1606	cccgaagaatgattgtgatatttttggctttagccttgaatattgaacatttcaacaatcct	1665
QY	1621	ggagtgaacttttctcctcgaatattgaacaacgctatggcgaagaagaagctgatttttt	1680
Db	1666	ggagtgaacttttctcctcgaatattgaacaacgctatggcgaagaagaagctgatttttt	1722
QY	1681	cacaaagggagaagcgttlaacaattgtcatcttcaaacatttggcctaataattatagtaca	1740

Db	1726	caaaaagggaagatggtaacaaaggtcacctccaacattctggccttaaatatatagtaca	1785
Qy	1741	cagaaatgttcaaaatcatagttttaaagtgttttgaagaagccacaaatatactta	1800
Db	1786	cagaatagtcaaaatcatagttttaaagtgttttgaagaagccacaaatatactta	1845
Qy	1801	tctttccttaataatcctgcgcaaatcctgcctgaaatccgaaatctgaaaaatgtactgyc	1860
Db	1846	tcttttcttaataatcctgcgcaaatcctgcctgaaatccgaaatctgaaaaatgtactgyc	1905
Qy	1861	tgaacaaaaattggtttgtgtgttgaggtatataacatataacttatcttattctgggtgt	1920
Db	1906	tgaacaaaaattggtttgtgtgttgaggtatataacatataacttatcttattctgggtgt	1965
Qy	1921	ttacgttatagccagttcccttctaattaaatctctgtttatataatttgaagtctt	1980
Db	1966	ttacgttatagccagttcccttctaattaaatctctgtttatataatttgaagtctt	2025
Qy	1981	tatagatcttctaataattctccttatagaaacatlaagaaaatcatlaactttaaata	2040
Db	2026	tatagatcttctaataattctccttatagaaacatlaagaaaatcatlaactttaaata	2085
Qy	2041	tacctaagcaaaaacatccaataagttataggttatgtccttattttcttaagc	2100
Db	2086	tacctaagcaaaaacatccaataagttataggttatgtccttattttcttaagc	2145
Qy	2101	tgaatacgatgacagcagtggtgtgaattctctgaaggaagtgaatgaatatattat	2160
Db	2146	tgaatacgatgacagcagtggtgtgaattctctgaaggaagtgaatgaatatattat	2205
Qy	2161	tcaagtggcaactttccaatttaccactgtacattattgtgtctcctgagttatacact	2220
Db	2206	tcaagtggcaactttccaatttaccactgtacattattgtgtctcctgagttatacact	2265
Qy	2221	aatttcagatatactcgtttaaattacacaaacagaagcaatttattgaagaattcgt	2280
Db	2266	aatttcagatatactcgtttaaattacacaaacagaagcaatttattgaagaattcgt	2335
Qy	2281	ttatcctcgcatgtccttggaaaaagcagcagaagaaacgaatttttgaactgtacagct	2340
Db	2326	ttatcctcgcatgtccttggaaaaagcagcagaagaaacgaatttttgaactgtacagct	2385
Qy	2341	ctgcgagagcatcttggttttctccttgctgtcttggtttccctacetttgaatcagattcgt	2400
Db	2386	ctgcgagagcatcttggttttctccttgctgtcttggtttccctacetttgaatcagattcgt	2445
Qy	2401	tttaagcagaagaacactcttggagacattcttgtaacctgaattcttttaattgc	2460
Db	2446	tttaagcagaagaacactcttggagacattcttgtaacctgaattcttttaattgc	2505
Qy	2461	atgaagtgtatitacatagcagaagtgtatgtattatctccctacacgtgtgaatc	2520
Db	2506	atgaagtgtatitacatagcagaagtgtatgtattatctccctacacgtgtgaatc	2563
Qy	2521	ctttgaactctgtcttgcgaatatggtgcagccacaaagggtgagata	2567
Db	2564	ctttgaactctgtcttgcgaatatggtgcagccacaaagggtgagata	2610

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RESULT 11
US-60-213-360-3302
; Sequence 3302, Application US/60213360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diiep, Dinah
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly
; TITLE OF INVENTION: Identified Therapy
; FILE REFERENCE: GX-0014 P
; CURRENT APPLICATION NUMBER: US/60/213,360
; CURRENT FILING DATE: 2000-06-21

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Db	1922	ttcagattctttaaattcccttctaagaacccaataatagaacattacattaaat	1981
QY	2040	ataccttiacagcaaaagcatccaanaatagaaglatagggltatgtcttattttctctcag	2099
Db	1982	ataccttiacagcaaaagcatccaanaatagaatagggltatgtcctattttctctcag	2041
QY	2100	ctgaatagcaatgaacacacagtggtggaatttctcgaagggaagcgatgaatatattat	2159
Db	2042	ctgaatagcaatgaacacacagtggtggaatttctcgaagggaagcgatgaatatattat	2101
QY	2160	ttcgaatgggcacttttccatttaccacgtaccattatttggttccctggagttacaac	2219
Db	2102	ttcgaatgggcacttttccatttaccacgtaccattatttggttccctggagttacaac	2161
QY	2220	taatttccagatbatactcgttcaaatlaccacaacacaaggaattatttgaagattccg	2279
Db	2162	taatttccagatbatactcgttcaaatlaccacaacacaaggaattatttgaagattccg	2221
QY	2280	ttatccctgcacatgtcttggaaaagcagagaaaagaatttttgaactgtatacgt	2339
Db	2222	ttatccctgcacatgtcttggaaaagcagagaaaagaatttttgaactgtatacgt	2281
QY	2340	tctgcaagagcacttctgttttcccttgccttctgttccctacccttgaatcagattccg	2399
Db	2282	tctgcaagagcacttctgttttcccttgccttctgttccctacccttgaatcagattccg	2341
QY	2400	ttttgctcaggaagaccttcttgggaccattcttagtaacctgaatttcccttttaattg	2459
Db	2342	ttttgctcaggaagaccttcttgggaccattcttagtaacctgaatttcccttttaattg	2401
QY	2460	catgaatgagatgtatcatcagcagaatgtagtggtatttccctccactggtgaatat	2519
Db	2402	catgaatgagatgtatcatcagcagaatgtagtggtatttccctccactggtgaatat	2460
QY	2520	cccttgaactgtcgttctgcaatatgtggcagccacaaaaggggagaga	2567
Db	2461	cccttgaactgtcgttcttcaatatgtggcagccacaaaagggtgagagata	2507
RESULT 12			
US-60-324-185-14440			
: Sequence 14440, Application US/60324185			
: GENERAL INFORMATION:			
: APPLICANT: Morris, Macdonald			
: APPLICANT: Lal, Preeti			
: APPLICANT: Diep, Dinh			
: TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING			
: TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE			
: FILE REFERENCE: GX-0019-1 P			
: CURRENT APPLICATION NUMBER: US/60/324,185			
: CURRENT FILING DATE: 2001-09-21			
: NUMBER OF SEQ ID NOS: 35862			
: SOFTWARE: PERL Program			
: SEQ ID NO 14440			
: LENGTH: 3446			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: FEATURE:			
: NAME/KEY: misc_feature			
: OTHER INFORMATION: Incyte ID NO: 221299.1			
US-60-324-185-14440			

Query Match	91.68;	Score 2448;	DB 71;	Length 3446;
Best Local Similarity	99.38;	Pred. No. 0;		
Matches 2490; Conservative	0;	Mismatches 15;	Indels 3;	Gaps 3;

[illegible][illegible]

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Db	1202	attttgcgaaagatctctgttaaacacctgtgagttcaatgtgtctgcgtggatctgcgtctcat	1261
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Qy	1381	ctcaagccaatgtttagaaggtttccccaagaatgtgataatgttttgccctcttgagaataa	1440
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Qy	1441	ttcccaagaagaataccagagactttacagagagcatccaccacaactctcaatgaaagtgc	1500
Db	1382	ttcccaagaagaagaataccagagactttacagagagagcatccaccacaactctcaatgaaagtgc	1441
Qy	1501	ttccctgtctgtatgagcatcagttatgtgttataatgaaataatgaaaccaactttaagatga	1560
Db	1442	ttccctgtctgtatgagcatcagttatgtgttataatgaaataatgaaaccaactttaagatga	1501
Qy	1561	cccgagaaatgtatgttgcattttttgtcattagccctgtgataatgtgaaactttcaacaatctct	1620
Db	1502	cccgagaaatgtatgttgcattttttgtcattagccctgtgataatgtgaaactttcaacaatctct	1561
Qy	1621	ggagtgactttttctcctctgcgaatgtgaacaacagttctatggcaagaagaagtgcatttttt	1680
Db	1562	ggagtgactttttctcctctgcgaatgtgaacaacagttctatggcaagaagaagtgcatttttt	1621
Qy	1681	cacaaagaaggagaacggttaacaatggtctacatctcaaaactttgggctaaattatattgtaca	1740
Db	1622	cacaaagaaggagaacggttaacaatggtctacatctcaaaactttgggctaaattatattgtaca	1681
Qy	1741	cagaaatgttccaaaatcaatagatttttaatgtgtttgaaaggccacacaatataacttta	1800
Db	1682	cagaaatgttccaaaatcaatagatttttaatgtgtttgaaaggccacacaatataacttta	1741
Qy	1801	tctttctcttaataatctct-gcaaatctctgcctctgatactcggaactctgaaatgtatgctg	1859
Db	1742	tctttctcttaataatctctgcgcaaatctctgcctggaatccggaactctgaaatgtatgctg	1801
Qy	1860	ctgtgaacaaaattgttttctgtgtgtatgagttataatcaatcaatcattatcttctgggtg	1919
Db	1802	ctgtgaacaaaattgttttctgtgtgtatgagttataatcaatcaatcattatcttctgggtg	1861
Qy	1920	tttagcttttaagccagttcctcttatatattttaaatcttctgttttatatatatttgaatgct	1979
Db	1862	tttagcttttaagccagttcctcttatatattttaaatcttctgttttatatatatttgaatgct	1921
Qy	1980	ttatagatttctcttaaatcttcccttatagagaaccttatagaanaatcatatcatatnaaat	2039
Db	1922	ttatagatttctcttaaatcttcccttatagagaaccttatagaanaatcatatcatatnaaat	1981
Qy	2040	ataccttaacagcaaaagcatccacaataagatagaggttattgtctctatatttctcttcag	2099
Db	1982	ataccttaacagcaaaagcatccacaataagatagaggttattgtctctatatttctcttcag	2041
Qy	2100	ctgaaatgcgaatgaacacagttgttggaattttcttgaagggaagtgtgtaaatatatattat	2159
Db	2042	ctgaaatgcgaatgaacacagttgttggaattttcttgaagggaagtgtgtaaatatatattat	2101
Qy	2160	ttcagttggcactctttccattcttataccacgttaccatatttgggtctccggaggtataaac	2219
Db	2102	ttcagttggcactctttccattcttataccacgttaccatatttgggtctccggaggtataaac	2161
Qy	2220	taattttcgaatataattctgtttaattaccacaacagaaggaacttattttgaaagattccg	2279
Db	2162	taattttcgaatataattctgtttaattaccacaacagaaggaacttattttgaaagattccg	2221
Qy	2280	tttatctctgcacattgcttttgaaaaaagcagcagaagaacgaatttttttgactgtatcagct	2339
Db	2222	tttatctctgcacattgcttttgaaaaaagcagcagaagaacgaatttttttttgactgtatcagct	2281

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OY 2340 tctgtagagacatcttctgttcttccttgccttctgttcttcctacatttgaaatccg 2399
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Db 2282 tctgcagagcatcttctgttcttccttgccttctgttcttcctacatttgaaatccg 2341
OY 2400 tttagtcagagaagactctctggagacattcttagtaacctgaattctcttttaattg 2459
      |||
Db 2342 ttctagtcagagaagactctctggagacattcttagtaacctgaattctcttttaattg 2401
OY 2460 catgaagtcgattgtatcatgagcaagtatggccttatttctccctacacgttgaaat 2519
      |||
Db 2402 catgaagtcgattgtatcatgagcaagtatggccttatttctccctacacgttgaaat 2460
OY 2520 cctttgaacttgcgtcttgcgaatatgaggcagccacaagaaggaggagaga 2567
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Db 2461 -cttgaacttgcgtcttgcgaatatgaggcagccacaagaaggaggagagata 2507

RESULT 13
; US-60-172-360-23662
; Sequence 23662, Application US/60172360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polym
; FILE REFERENCE: GX-0007 P
; CURRENT APPLICATION NUMBER: US/60/172,360
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 29838
; SOFTWARE: PERL Program
; SEQ ID NO 23662
; LENGTH: 3393
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 221299.1
US-60-172-360-23662

Query Match 91.5%; Score 2446.4; DB 56; Length 3393;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 2489; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

OY 61 ggcgtgtcccgctctgcgcccgacgcccctcgatctcccgctgacttccctgcgcaggcg 120
Db 2 ggcgtgtcccgctctgcgcccgacgcccctcgatctcccgctgacttccctgcgcaggcg 61
OY 121 cctgtgcctctcgggacacattgtgcgtctgcgcgggaattcgctgcgcccgcgct 180
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Db 62 cctgtgcctctcgggacacattgtgcgtctgcgcgggaattcgctgcgcccgcgct 121
OY 181 gccaggaacgcgagacagacgcgcgtacacgagacccttccagacacttgagccgaatg 240
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Db 122 gccaggaacgcgagacagacgcgcgtacacgagacccttccagacacttgagccgaatg 181
OY 241 gggacgagctgtgtgacatcggcgagctgcagagcgggctcaagaaacctggcatccctc 300
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Db 182 gggacgagctgtgtgacatcggcgagctgcagaggggctcagaacctggcatccctc 241
OY 301 tgggcacgaagcccgagagagaataatttactactcggagatgtcaacaagaatggaagc 360
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Db 242 tgggcacgaagcccgagagagaataatttactactcggagatgtcaacaagaatggaagc 301
OY 361 tggatttcgaagaattcttcgaagtaaccttaagaagccatgagaaagaaatggaattggcat 420
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Db 302 tggatttcgaagaattcttcgaagtaaccttaagaagccatgagaaagaaatggaattggcat 361
OY 421 ttaagagtttagacaaaaataatgatvgaaaaaattgaggtcttcgaattgttccagttc 480
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Db 362 ttaagagtttagacaaaaataatgatvgaaaaaattgaggtcttcgaattgttccagttc 421

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QY 481 tccagacactggtctgaactatttctgaacaacagcagatgtattcttccaagcattg 540  
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Db 422 tccagacactggtctgaactatttctgaacaacagcagatgtattcttccaagcattg 481  
QY 541 atgttgaatggacaatgacagctgagctggaatgaaatggagagactacttcttaatac 600  
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Db 482 atgttgaatggacaatgacagctgagctggaatgaaatggagagactacttcttaatac 541  
QY 601 ctgtttaaagcatttgaagaatataccgtttcttgaacaattcctacaggaattgacatag 660  
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Db 542 ctgtttaaagcatttgaagaatataccgtttcttgaacaattcctacaggaattgacatag 601  
QY 661 gggaatacctaactatccagatgaatctcagcagagacgaaaaaaatcccgacaatggt 720  
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Db 602 gggaatacctaactatccagatgaatctcagcagagacgaaaaaaatcccgacaatggt 661  
QY 721 ggagcagacttctgagcagagcattgctgctgctctcagacaagcctgccccct 780  
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Db 662 ggagcagacttctgagcagagcattgctgctgctctcagacaagcctgccccct 721  
QY 781 tggacgcttcgaaaatcatgatacgagttcaagttcaaaatcagacaataatgacatat 840  
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Db 722 tggacgcttcgaaaatcatgatacgagttcaagttcaaaatcagacaataatgacatat 781  
QY 841 ttggtgcttcgacagatgtiaaagaagaggtatccgctgcttggaggggaatg 900  
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Db 782 ttggtgcttcgacagatgtiaaagaagaggtatccgctgcttggaggggaatg 841  
QY 901 gtacaacgctcatcaaaatgtctcctctgagacagctgttaaatctcggacatatgaacagt 960  
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Db 842 gtacaacgctcatcaaaatgtctcctctgagacagctgttaaatctcggacatatgaacagt 901  
QY 961 acaagaagtacttacttactgaaagaagaaacaaaatagaaacatttgaagatttctctg 1020  
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Db 902 acaagaagtacttacttactgaaagaagaaacaaaatagaaacatttgaagatttctctg 961  
QY 1021 gttccatgcttgagcagcactgacagactttatataccaatgaggtatgtaaacca 1080  
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Db 962 gttccatgcttgagcagcactgacagactttatataccaatgaggtatgtaaacca 1021  
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Db 1022 ggtctgctgttagcnaaaactgagcagctactctggaatataatgattgtgccaagaagatt 1081  
QY 1141 tgaacaatgaaagcttggaggtttttacaaggtctatgttcccaatttataggtatca 1200  
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QY 1261 attttgcaaaaagattctgtataacccttggagtcagtgtgtctgtaggaatggcggtccttat 1320  
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Db 1202 attttgcaaaaagattctgtataacccttggagtcagtgtgtgtgtaggaatggcggtccttat 1261  
QY 1321 ccaagcactgtgtgtagcgttgcagctacacccatttggcttggtagaactccgatgagag 1380  
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Db 1262 ccaagcactgtgtgtagcgttgcagctacacccatttggcttggtagaactccgatgagag 1321  
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QY 1441 ttctccaaagaagaataccaggaacttaccagaggtatccaccccaacttaccagaggtgc 1500  
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Db 1382 ttctccaaagaagaataccaggaacttaccagaggtatccaccccaacttaccagaggtgc 1441  
QY 1501 tccctgtgtgaggtacatagttatgtgttatgaaataatgaaagcaacttggagtaaa 1560  
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QY 1561 cccaagaatgatagttgcatttttgcctttaagcctgataataatgaaacttccaacaactct 1620  
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Db 1502 cccaagaatgatagttgcatttttgcctttaagcctgataataatgaaacttccaacaactct 1561  
QY 1621 ggaatgacttttctcctcgaattgaaacaagtctatgagcaaaaagaactgcatttttt 1680  
|||||  
Db 1562 ggaatgacttttctcctcgaattgaaacaagtctatgagcaaaaagaactgcatttttt 1621  
QY 1681 cacaagaaggagacggtgaacaagtgtcacttccaacttttgggttaattatataatgata 1740  
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Db 1622 cacaagaaggagatgtaacaagtgtcacttccaacttttgggttaattatataatgata 1681  
QY 1741 cagaatgttcaaatcatagtttaatgtgttttgaagaagccacaattatattctta 1800  
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Db 1682 cagaatgttcaaatcatagtttaatgtgttttgaagaagccacaattatattctta 1741  
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Db 1742 tcttttcttaataatcctgcaaatctctgcctgaaatccgaaatctgaaatgtactg 1801  
QY 1860 ctgaaacaaaattggttgtgtgttagagttataaataatcattatcttattcggtg 1919  
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Db 1802 ctgaaacaaaattggttgtgtgttagagttataaataatcattatcttattcggtg 1861  
QY 1920 tttaagtttagccagttcccttataatttataatttctgtttatataatttgaatgtct 1979  
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Db 1862 tttaagtttagccagttcccttataatttataatttctgtttatataatttgaatgtct 1921  
QY 1980 ttatagatttctttaaatttccctataagaaacatlaaagaataatcattatcttaaat 2039  
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Db 1922 ttatagatttctttaaatttccctataagaaacatlaaagaataatcattatcttaaat 1981  
QY 2040 atacttaacgcaaaaagcatcccaataatagataaggtttatgtccttattttcttttag 2099  
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Db 1982 atacttaacgcaaaaagcatcccaataatagataaggtttatgtccttattttcttttag 2041  
QY 2100 ctgataacgaatgaaacagagtggtggaattctcgaaggaggtgataatataattat 2159  
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Db 2042 ctgataacgaatgaaacagagtggtggaattctcgaaggaggtgataatataattat 2101  
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Db 2102 ttcaatggagcatttccatttcaacatttcaacattatgttgcctgaggtatacac 2161  
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Db 2162 taatttccagatatacttactgtttaaattataccaacaagcgaattatatttgaagaattccg 2221  
QY 2280 ttatctcctgcatgtcttgaagaagcagcagaaacgaatatttgaactgtatcaact 2339  
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Db 2222 ttatctcctgcatgtcttgaagaagcagcagaaacgaatatttgaactgtatcaact 2281  
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Db 2342 tttaagtcaggaagaacttcttggagcaacttcttgaataaccgaatattctttttaattg 2401  
QY 2460 catgaagtgtatgatcatgagcagatgaggtttatcttccctcactcaggtgaataat 2519  
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Db 2461 -ccttgaactgtctgttgaataatgagcagcacaagaaggagagagata 2507

RESULT 14  
US-60-278--561-5850  
; Sequence 5850, Application US/60278561  
; GENERAL INFORMATION:

APPLICANT: Morris, MacDonald  
APPLICANT: Lal, Preeti  
APPLICANT: Diep, Dinh  
TITLE OF INVENTION: Method for the identification of sequence polymorphisms using  
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide  
TITLE OF INVENTION: Polymorphisms Identified Thereby  
FILE REFERENCE: GX-0012-1-P  
CURRENT APPLICATION NUMBER: US/60/278,561  
CURRENT FILING DATE: 2001-03-23  
NUMBER OF SEQ ID NOS: 15598  
SOFTWARE: PERL Program  
SEQ ID NO 5850  
LENGTH: 3446  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc.feature  
OTHER INFORMATION: Incyte ID No: 221299.1  
US-60-278-561-5850

Query Match 91.5%; Score 2446.4; DB 66; Length 3446;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 2489; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

QY 61 ggcgtgctccggtctcgcgccgagccctcgatctcccgtagactctccgcagagcg 120  
DB 2 ggcgtgctccggtctcgcgccgagccctcgatctcccgtagactctccgcagagcg 61  
QY 121 cctggccctctgggacacatgttcgtgctgtggagactcgcgcggccacagcgccct 180  
DB 62 cctggccctctgggacacatgttcgtgctgtggagactcgcgcggccacagcgccct 121  
QY 181 gccacgacgcggagcagccgacgcgctacgagacccctctccagcacttggacgcgaatg 240  
DB 122 gccacgacgcggagcagccgacgcgctacgagacccctctccagcacttggacgcgaatg 181  
QY 241 gggagcgaatgtgtgacacatcgcgcgagctgcaaggagggtctcaagaaacctgggcatccctc 300  
DB 182 gggagcgaatgtgtgacacatcgcgcgagctgcaaggagggtctcaagaaacctgggcatccctc 241  
QY 301 tgggccaagacgcccgaaggaaaatttttactacttggagatgtccaacaagaatggggaagc 360  
DB 242 tgggccaagacgcccgaaggaaaatttttactacttggagatgtccaacaagaatggggaagc 301  
QY 361 tggatttgaagaattatgaagtacaccttaagaacacatgagaagaataatgtgcat 420  
DB 302 tggatttgaagaattatgaagtacaccttaagaacacatgagaagaataatgtgcat 361  
QY 421 ttaagagtttagaacaataatgatgtgaaaatvtgaggtctcagaatvtgtccagcttc 480  
DB 362 ttaagagtttagaacaataatgatgtgaaaatvtgaggtctcagaatvtgtccagcttc 421  
QY 481 tccaagacatgtggttgcactatttcttgcacaacaagcagaatgttcttcaagaatgtg 540  
DB 422 tccaagacatgtggttgcactatttcttgcacaacaagcagaatgttcttcaagaatgtg 481  
QY 541 atgttgaatggagaacatgacagtgtagcttgaatgaatgagagactacttcttaataac 600  
DB 482 atgttgaatggagaacatgacagtgtagcttgaatgaatgagagactacttcttaataac 541  
QY 601 ctgttcaacacatgagaaatataccgttcttgcagaacattctacaggaattgacatag 660  
DB 542 ctgttcaacacatgagaaatataccgttcttgcagaacattctacaggaattgacatag 601  
QY 661 gggatagcttaactatctcagatgaatttccaggaagacgaaaaaaatttcggacaatgtg 720  
DB 602 gggatagcttaactatctcagatgaatttccaggaagacgaaaaaaatttcggacaatgtg 661  
QY 721 ggaagcagcttcttgcaggaagcagcatgtcgtgtctctctcgaaaaagcagtcgccct 780  
DB 662 ggaagcagcttcttgcaggaagcagcatgtcgtgtctctctcgaaaaagcagtcgccct 721

QY 781 tggaccgtctgtaaaatcatatgacaggttcaacggttcaaaatcagaacaataatgacatat 840  
DB 722 tggaccgtctgtaaaatcatatgacaggttcaacggttcaaaatcagaacaataatgacatat 781  
QY 841 ttgttgcttctcagacatgagtgtaaaagaagagtgctccgtctgttggaggaggaatg 900  
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QY 901 gtacaacgtcacaacaatatgtctcctgagacagcttcaatctgtgcatatgacaagt 960  
DB 842 gtacaacgtcacaacaatatgtctcctgagacagcttcaatctgtgcatatgacaagt 901  
QY 961 acaagaagtactactatgagaagaagacaacaataatgagaacatttggagattattctgt 1020  
DB 902 acaagaagtactactatgagaagaagacaacaataatgagaacatttggagattattctgt 961  
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QY 1321 ccagcaccgtgtgtcaagcttgcgcagctaccacattgtgctgtgagaactcgcattgcagg 1380  
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QY 1381 ctcaagcactgttagaaggttccccaagctggaatgtgttgccctcttcgacgaatta 1440  
DB 1322 ctcaagcactgttagaaggttccccaagctggaatgtgttgccctcttcgacgaatta 1381  
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DB 1682 cagaagtgtcacaatatcatagtttaagtgtgttgaagaaggccaacaattatattctta 1741  
QY 1801 tcttttcttaataactc-gcaaatctgcgcctggaatccgaatctgaaaaatgttactgg 1859  
DB 1742 tcttttcttaataactcctggaatctgcgcctggaatccgaatctgaaaaatgttactgg 1801  
QY 1860 ctggaacaataattgttctgtgtgttagagttataaaatcattatatttgggtgg 1919





QY 908 cgtcatcaaaaattgctctctgaagacagctgttaaatctctgggcaatgaacagtaacagaa 967  
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Db 883 cgtcatcaaaaattgctctctgaagacagctgttaaatctctgggcaatgaacagtaacagaa 942  
QY 968 gttacttactgaaagaaagaaacaaaataagaaacatttgaaagatttattctgttccat 1027  
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Db 943 gttacttactgaaagaaagaaacaaaataagaaacatttgaaagatttattctgttccat 1002  
QY 1028 ggtctggagcaactgcacagactttatataatccaatggaggttatgaaacccggctgac 1087  
|||||  
Db 1003 ggtctggagcaactgcacagactttatataatccaatggaggttatgaaacccggctgac 1062  
QY 1088 tgttagcaaaaactcggcagtaactctcggaaatataatgtgtgtccagaagaatttgaaca 1147  
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Db 1063 tgttagcaaaaactcggcagtaactctcggaaatataatgtgtgtccagaagaatttgaaca 1122  
QY 1148 tgaaggtctggaggtctttttacaagaagctatgttcccaatttatgtgtatccatctta 1207  
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Db 1123 tgaaggtctggaggtctttttacaagaagctatgttcccaatttatgtgtatccatctta 1182  
QY 1208 tgcagagcatagatctctgtctgtatagctcttgaagctccatctgtgataatttgc 1267  
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Db 1183 tgcagagcatagatctctgtctgtatagctcttgaagctccatctgtgataatttgc 1242  
QY 1268 aaaaatctcgtlaaacccctggagtcatactgtctcggagatgcgtgtcccttaccagcac 1327  
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Db 1243 aaaaatctcgtlaaacccctggagtcatactgtctcggagatgcgtgtcccttaccagcac 1302  
QY 1328 ctgtgttcaagctctgcagacttaacccatctgtcttgggtgagaactccgcatgtgaagctcaagc 1387  
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Db 1303 ctgtgttcaagctctgcagacttaacccatctgtcttgggtgagaactccgcatgtgaagctcaagc 1362  
QY 1388 catgttagaagagttccccaagctgtgaatagtctgcctcttccgaacgaattttccca 1447  
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Db 1363 catgttagaagagttccccaagctgtgaatagtctgcctcttccgaacgaattttccca 1422  
QY 1448 agaagaataacaggaacttaacagagcatcaccccaactcaatgaagtgctccctgc 1507  
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Db 1423 agaagaataacaggaacttaacagagcatcaccccaactcaatgaagtgctccctgc 1482  
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Db 1483 tctagagcatagttatgtgtttatgaaaaatgatgaagcaaaactttggaggttaacccaaga 1542  
QY 1568 atgatgttgcaattttgtcttagcctgaatgaactttcaacaactctcggagtga 1627  
|||||  
Db 1543 atgatgttgcaattttgtcttagcctgaatgaactttcaacaactctcggagtga 1602  
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Db 1603 cttttctcctcgaattgaaacaagtctatgccaagaagaagctgcaatttttccacaaa 1662  
QY 1688 ggggaagcgttaacaaatgtgtcaacttcaaaactttgggtcaaatatgatgtacacagaat 1747  
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Db 1663 ggggaagcgttaacaaatgtgtcaacttcaaaactttgggtcaaatatgatgtacacagaat 1722  
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QY 1928 tatgcaggtctcttaataatctctgtgtttatatacatcttgaagtctctataagat 1987  
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Db 2443 ggaattgatcagcagagtgagtttatcttccctcactggtgaaatcccttga 2500  
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Search completed: August 18, 2002, 09:16:00  
J00 Time: 9204 sec



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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2002, 07:16:56 ; Search time 404.19 Seconds  
(Without alignments)  
17287.517 Million cell updates/sec

Title: US-09-777-921A-1  
Perfect score: 2673  
Sequence: 1 ccgaaccccgagcgagccccc.....ataccatgcatgattctg 2673

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1664314 seqs, 1307041093 residues

Total number of hits satisfying chosen parameters: 3328628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Pending\_Patents\_NA\_New.\*

1: /cgn2\_6/ptodata1/pna/PCT\_NEW\_COMB.seq.\*  
2: /cgn2\_6/ptodata1/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata1/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata1/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata1/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata1/pna/US10\_NEW\_COMB.seq2.\*  
8: /cgn2\_6/ptodata1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2673	100.0	2673	US-09-777-921A-1	Sequence 1, Appl1
2	2428	90.8	3384	US-09-620-325-408	Sequence 408, App
3	1135	42.5	69327	US-09-777-921A-3	Sequence 3, Appl1
4	933.8	34.9	1839	US-09-919-002-4478	Sequence 4478, Ap
5	730.8	27.3	757	US-10-158-057-38	Sequence 38, Appl
6	597.4	22.3	601	US-09-777-921A-120	Sequence 120, App
7	597.4	22.3	601	US-09-777-921A-121	Sequence 121, App
8	545.4	20.4	1808	US-10-152-661-454	Sequence 454, App
9	545.4	20.4	1816	US-09-312-838-262	Sequence 262, App
10	545.4	20.4	1816	US-10-152-661-262	Sequence 262, App
11	543.8	20.3	3334	US-09-991-150-288	Sequence 288, App
12	543.8	20.3	3334	US-10-063-510-57	Sequence 57, Appl
13	543.8	20.3	3334	US-10-063-512-57	Sequence 57, Appl
14	543.8	20.3	3334	US-10-063-513-57	Sequence 57, Appl
15	543.8	20.3	3334	US-10-063-514-57	Sequence 57, Appl
16	543.8	20.3	3334	US-10-063-515-57	Sequence 57, Appl
17	543.8	20.3	3334	US-10-063-516-57	Sequence 57, Appl
18	543.8	20.3	3334	US-10-063-517-57	Sequence 57, Appl
19	543.8	20.3	3334	US-10-063-518-57	Sequence 57, Appl
20	543.8	20.3	3334	US-10-063-519-57	Sequence 57, Appl
21	543.8	20.3	3334	US-10-063-520-57	Sequence 57, Appl
22	543.8	20.3	3334	US-10-063-521-57	Sequence 57, Appl
23	543.8	20.3	3334	US-10-063-522-57	Sequence 57, Appl
24	543.8	20.3	3334	US-10-063-523-57	Sequence 57, Appl
25	543.8	20.3	3334	US-10-063-524-57	Sequence 57, Appl

26	543.8	20.3	3334	US-10-063-525-57	Sequence 57, Appl
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29	543.8	20.3	3334	US-10-063-528-57	Sequence 57, Appl
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32	543.8	20.3	3334	US-10-063-531-57	Sequence 57, Appl
33	543.8	20.3	3334	US-10-063-532-57	Sequence 57, Appl
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35	543.8	20.3	3334	US-10-063-534-57	Sequence 57, Appl
36	543.8	20.3	3334	US-10-063-535-57	Sequence 57, Appl
37	543.8	20.3	3334	US-10-063-536-57	Sequence 57, Appl
38	543.8	20.3	3334	US-10-063-537-57	Sequence 57, Appl
39	543.8	20.3	3334	US-10-063-538-57	Sequence 57, Appl
40	543.8	20.3	3334	US-10-063-539-57	Sequence 57, Appl
41	543.8	20.3	3334	US-10-063-540-57	Sequence 57, Appl
42	543.8	20.3	3334	US-10-063-541-57	Sequence 57, Appl
43	543.8	20.3	3334	US-10-063-542-57	Sequence 57, Appl
44	543.8	20.3	3334	US-10-063-543-57	Sequence 57, Appl
45	543.8	20.3	3334	US-10-063-544-57	Sequence 57, Appl

## ALIGNMENTS

RESULT 1  
US-09-777-921A-1  
Sequence 1, Application US/0977921A  
GENERAL INFORMATION:  
APPLICANT: MERKULOV et al.  
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
TITLE OF INVENTION: AND USES THEREOF  
FILE REFERENCE: C1001103  
CURRENT APPLICATION NUMBER: US/09/777, 921A  
CURRENT FILING DATE: 2002-02-07  
NUMBER OF SEQ ID NOS: 126  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 1  
LENGTH: 2673  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-777-921A-1

Query Match	Best Local Similarity	Score	DB 5:	Length	2673:
Matches 2673;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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Db 1		100.0%;	2673;	DB 5:	Length 2673;
QY 61		100.0%;	2673;	DB 5:	Length 2673;
Db 61		100.0%;	2673;	DB 5:	Length 2673;
QY 121		100.0%;	2673;	DB 5:	Length 2673;
Db 121		100.0%;	2673;	DB 5:	Length 2673;
QY 181		100.0%;	2673;	DB 5:	Length 2673;
Db 181		100.0%;	2673;	DB 5:	Length 2673;
QY 241		100.0%;	2673;	DB 5:	Length 2673;
Db 241		100.0%;	2673;	DB 5:	Length 2673;
QY 301		100.0%;	2673;	DB 5:	Length 2673;
Db 301		100.0%;	2673;	DB 5:	Length 2673;

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QY 601 ctgttaacagacattvgaagaaattatccggttcttcgaaacacttcaagaaattagaacatag 660  
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Db 601 ctgttaacagacattvgaagaaattatccggttcttcgaaacacttcaagaaattagaacatag 660  
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QY 1381 ctcaagccatvgttgaagaagttccccaacagctgaatalvgttvtggtccttccgaagatla 1440  
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Db 1441 ttcccaaaaagaagaataccagaagactttagagagcatcaccaccaacttcaagaaggtgc 1500  
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Qy	2561	ggcggggtgtacatgaactcttgcgaacatgtgataccctatttgcgaaggggaagccca	2640
Db	2561	ggcggggtgtacatgaactcttgcgaacatgtgataccctatttgcgaaggggaagccca	2640
Qy	2641	tttggggaacatataccaatgatgatattctgt	2673
Db	2641	tttggggaacatataccaatgatgatattctgt	2673

RESULT 2  
HS-09-620-325-408

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Sequence 408, Application US/09620325
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wehrman, Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Yungqing
APPLICANT: Wang, Dunrui
APPLICANT: Tillinghast, John
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: Polypeptides
CURRENT APPLICATION NUMBER: 787C1P2B
CURRENT FILING DATE: US/09/620,325
PRIOR APPLICATION NUMBER: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 419
SOFTWARE: pt_FL-genes Version 1.0
SEQ ID NO 408
LENGTH: 3384
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (113)..(1546)
US-09-620-325-408

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[illegible]

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Oy	368	tgaagaatttgaagtaaccttaagaagccgtgaagaagaatvtgaatttgcattgaag	427
Dh	343	tgaagaatttctgaagtaaccttaagaagccgtgaagaagaatvtgaatttgcattgaag	402
Oy	428	tttaagacaanaataatgaatgaanaaattgagcttcaagaatvtgccagtcctccagac	487
Dh	403	tttagacaanaataatgaatgaanaaattgagcttcaagaatvtgccagtcctccagac	462
Oy	468	actggtcttgactcttcttgaacaacaagcagaattgattcttcaagaatvtgta	547
Dh	463	actggtcttgactcttcttgaacaacaagcagaattgattcttcaagaatvtgta	522
Oy	548	tgggaacaatgacagtgaagcttggaatgaatgaagaagctcttcttaatcccgttac	607
Dh	523	tgggaacaatgacagtgaagcttggaatgaatgaagaagctcttcttaatcccgttac	582
Oy	608	agacatttgaagaaattacccgttctcttgaacaacttcaagaagaatvtgataagggatag	667
Dh	583	agacatttgaagaaattacccgttctcttgaacaacttcaagaagaatvtgataagggatag	642
Oy	668	cttaactatccagaatgaattcaacggaagaagcaaaaaatccggaacaatvtgtgaagca	727
Dh	643	cttaactatccagaatgaattcaacggaagaagcaaaaaatccggaacaatvtgtgaagca	702
Oy	728	gcttttggcaggaagcattgctgtgctgtctctgaacaagcagctccctttgacgg	787
Dh	703	gcttttggcaggaagcattgctgtgctgtctctctgaacaagcagctccctttgacgg	762
Oy	788	lctgaanaatcctgaatgaaggttcaacggttccaatacagaacaatvtgaacatacttggtg	847
Dh	763	lctgaanaatcctgaatgaaggttcaacggttccaatacagaacaatvtgaacatacttggtg	822
Oy	848	ctttcgcacagaatgttaaagaagaaggtatccgctccgtcttggaggggaaatvtgtacaa	907
Dh	823	ctttcgcacagaatgttaaagaagaaggtatccgctccgtcttggaggggaaatvtgtacaa	882
Oy	908	cgtaacaanaattgtctctctgaagcagctgtttaattcttggagatltgaacagttacaaga	967
Dh	883	cgtaacaanaattgtctctctgaagcagctgtttaattcttggagatltgaacagttacaaga	942
Oy	968	gttaacttactgaagaagaacaanaaattagaagaacttgaagaatttatcttcggttcat	1027
Dh	943	gttaacttactgaagaagaagaacaanaaattagaagaacttgaagaatttatcttcggttcat	1002
Oy	1028	ggctcgtgaagcaactcgcacagaacttltatataccaatlgagaagtltatgaanaaccagctgcg	1087
Dh	1003	ggctcgtgaagcaactcgcacagaacttltatataccaatlgagaagtltatgaanaaccagctgcg	1062
Oy	1088	tgtatgacaanaacttgggagcagtaacctcgtgaatatatgtatttgcgaagaagaatttgaaca	1147
Dh	1063	tgtatgacaanaacttgggagcagtaacctcgtgaatatatgtatttgcgaagaagaatttgaaca	1122
Oy	1148	tgaagccttgggaagcttttacaagaagctatgttccaattatattaggtatcatacctta	1207
Dh	1123	tgaagccttgggagcttttacaagaagctatgttccaattatattaggtatcatacctta	1182
Oy	1208	tgcagcagatagatcttgcgtgtatagagctcttgaagctccatctgcgtgaataatttgc	1267
Dh	1183	tgcagcagatagatcttgcgtgtatagagctcttgaagctccatcttgcgtgaataatttgc	1242
Oy	1268	aaaagaattctgttaaacctctggagtcagtgtgtgtgcctgggaatgagctgcttatccagac	1327
Dh	1243	aaaagaattctgttaaacctctggagtcagtgtgtgtgcctgggaatgagctgcttatccagac	1302
Oy	1328	ctgctggtcagaactgcccagcagccacccatttggcttgggtgaanaatcgcagcagggcccaagc	1387
Dh	1303	ctgctggtcagaactgcccagcagccacccatttggcttgggtgaanaatcgcagcagggcccaagc	1362
Oy	1388	catgttgaagaagttccccaagctgtgaatatgttgtgctctcttgcagcaatbatttccaa	1447

Db 1363 catgttagaaggtccccacagctgaatagtgtgctcttcgcagcaattattccaa 1422  
QY 1448 agaagaatacacagagacttacagagcatcaccccaaatcattaaagtgctccctgc 1507  
Db 1423 agaagaatacacagagacttacagagcatcaccccaaatcattaaagtgctccctgc 1482  
QY 1508 tctagagcatcagttatgtgtttatgaataatagaagcaactttgaggttaaccagaa 1567  
Db 1483 tctagagcatcagttatgtgtttatgaataatagaagcaactttgaggttaaccagaa 1542  
QY 1568 atgagttgcatcttttgcctttagctgtaatttgaacttttcaaacctctcgaggtga 1627  
Db 1543 atgagttgcatcttttgcctttagctgtaatttgaacttttcaaacctctcgaggtga 1602  
QY 1628 cttttctcctcgaaattgaacaagctctatgagcaaaagagctgtcatcttttcaaaaa 1687  
Db 1603 cttttctcctcgaaattgaacaagctctatgagcaaaagagctgtcatcttttcaaaaa 1662  
QY 1688 ggggaagaggttaacaaatgtctacatcaaacctttgggctaaattatgttacaagaaat 1747  
Db 1663 ggggaagaggttaacaaatgtctacatcaaacctttgggctaaattatgttacaagaaat 1722  
QY 1748 gtccaataatcagatttttaattgtgttttgaagaagccacaaattatcttattcttttc 1807  
Db 1723 gtccaataatcagatttttaattgtgttttgaagaagccacaaattatcttattcttttc 1782  
QY 1808 ttaataatcctgcaaaatctctgacctgaatccgaaatctgaaatgttactggttgaaca 1867  
Db 1783 ttaataatcctgcaaaatctctgacctgaatccgaaatctgaaatgttactggttgaaca 1842  
QY 1868 aaattgtttgtgtgtgtgaagttataaatcaatcaatttattctcggtgtgttgcgtt 1927  
Db 1843 aaattgtttgtgtgtgtgaagttataaatcaatcaatttattctcggtgtgttgcgtt 1902  
QY 1928 tatgcaggttccctttatattaaattctgtgtttatattatatttgaatttccttataagt 1987  
Db 1903 tatgcaggttccctttatattaaattctgtgtttatattatatttgaatttccttataagt 1962  
QY 1988 ttctttaaatcttccatataagaacattataagaanaatcaatcaatttaataatactta 2047  
Db 1963 ttctttaaatcttccatataagaacattataagaanaatcaatcaatttaataatactta 2022  
QY 2048 cagcaaaagcatcccaataagttataggtttatgtcccttaatttcttccagctgaatc 2107  
Db 2023 cagcaaaagcatcccaataagttataggtttatgtcccttaatttcttccagctgaatc 2082  
QY 2108 ggaatgaacacagtggtggaattctctgaagggaagtgaataattatattatttgaagt 2167  
Db 2083 ggaatgaacacagtggtggaattctctgaagggaagtgaataattatattatttgaagt 2142  
QY 2168 gcaactttccatttaccactgtacattattgtgtccctgaggtatatacaactatttc 2227  
Db 2143 gcaactttccatttaccactgtacattattgtgtccctgaggtatatacaactatttc 2202  
QY 2228 agtatattactgtttaataatcaacaacaggaatttatttgaagaattccggtttacct 2287  
Db 2203 agtatattactgtttaataatcaacaacaggaatttatttgaagaattccggtttacct 2262  
QY 2288 ggcattgtcttgaagaagcaggaagaagaatttttgaactgtatcagctcttcagaa 2347  
Db 2263 ggcattgtcttgaagaagcaggaagaagaatttttgaactgtatcagctcttcagaa 2322  
QY 2348 gcaacttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 2407  
Db 2323 gcaacttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 2382  
QY 2408 aggaagaactcttggagacatccctgaatgaactgaacttcttcttcttcttcttcttct 2467  
Db 2383 aggaagaactcttggagacatccctgaatgaactgaacttcttcttcttcttcttcttct 2442  
QY 2468 ggaattatcatatgaagaagtgaggtgtatttcttccctcactggtgaattcctttga 2527  
Db 2443 ggaattatcatatgaagaagtgaggtgtatttcttccctcactggtgaattcctttga 2500

QY 2528 ctgtctgtttgcaatattggtgcagccacaaagggtgagaga 2567  
Db 2501 ctgtctgtttgcaatattggtgcagccacaaagggtgagaga 2540

## RESULT 3

US-09-777-921A-3  
; Sequence 3, Application US/09777921A  
; GENERAL INFORMATION:  
; APPLICANT: MERKULOV et al.  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS.  
; TITLE OF INVENTION: NOCTURNAL ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS.  
; FILE REFERENCE: CLO01103  
; CURRENT APPLICATION NUMBER: US/09/777,921A  
; CURRENT FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 126  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 69327  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(69327)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-777-921A-3

Query Match 42.5%; Score 1135; DB 5; Length 69327;  
Best Local Similarity 98.6%; Pred. No. 4.3e-223;  
Matches 1166; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

QY 1385 agccatgttagaaggtccccacagctgaatagtgtgctcttcgcagcaattattcc 1444  
Db 66163 agccatgttagaaggtccccacagctgaatagtgtgctcttcgcagcaattattcc 66222  
QY 1445 caaagaagaatacacagagacttacagagcatcaccccaaatcattaaagtgctccc 1504  
Db 66223 caaagaagaatacacagagacttacagagcatcaccccaaatcattaaagtgctccc 66282  
QY 1505 tgcgtgagcatcagttatgtgtttatgaataatagaagcaactttgaggttaacc 1564  
Db 66283 tgcgtgagcatcagttatgtgtttatgaataatagaagcaactttgaggttaacc 66342  
QY 1565 ggaatgaatcagatttttgcctttagcctgtgaatttgaactttcaaacctctcgag 1624  
Db 66343 ggaatgaatcagatttttgcctttagcctgtgaatttgaactttcaaacctctcgag 66402  
QY 1625 tgactttctcctcgaaattgaacaagctctatgagcaaaagagctgtcatcttttccaa 1684  
Db 66403 tgactttctcctcgaaattgaacaagctctatgagcaaaagagctgtcatcttttccaa 66462  
QY 1685 aaaaggaagaggttaacaaatgtctacatcaaacctttgggctaaattatataatgaacaga 1744  
Db 66463 aaaaggaagaggttaacaaatgtctacatcaaacctttgggctaaattatataatgaacaga 66522  
QY 1745 aatgttcaaaatcagattttaaattgtgtttgaagaagccacaaattatatttacct 1804  
Db 66523 aatgttcaaaatcagattttaaattgtgtttgaagaagccacaaattatatttacct 66582  
QY 1805 ttcttaataatcctgcaaatctctgcctgaaatccgaaatcgtgaatgttactgtctga 1864  
Db 66583 ttcttaataatcctgcaaatctctgcctgaaatccgaaatcgtgaatgttactgtctga 66642  
QY 1865 acaaaattgtttgtgtgtgtgaagttataatcaatcaatcttattcttccggtggttac 1924  
Db 66643 acaaaattgtttgtgtgtgtgaagttataatcaatcaatcttattcttccggtggttac 66702  
QY 1925 gttttgcaggttcccttattatatttatttctgtttattatatttgaattgttcttata 1984  
Db 66703 gttttgcaggttcccttattatatttatttctgtttattatatttgaattgttcttata 66762



QY 1985 gatttcttaattcccttataagaaccttaataagaataatcatatataatataacc 2044  
|||||  
Db 66763 gatttcttaattcccttataagaaccttaataagaataatcatatataatataacc 66822  
QY 2045 ttacagcaaaaagcaccacaataaglataggttatgttccctatttcttccagcgaa 2104  
|||||  
Db 66823 ttacagcaaaaagcaccacaataaglataggttatgttccctatttcttccagcgaa 66882  
QY 2105 taagaatgaacacagtggttggaattcttgaagggaagtgaatataatattatccag 2164  
|||||  
Db 66883 taagaatgaacacagtggttggaattcttgaagggaagtgaatataatattatccag 66942  
QY 2165 tgggcaatttccatttaccacgtacacatttggttccctggaggtataacataatt 2224  
|||||  
Db 66943 tgggcaatttccatttaccacgtacacatttggttccctggaggtataacataatt 67002  
QY 2225 ttcaatataactgttaataataccacaacaggaattatattgaagaattccgattat 2284  
|||||  
Db 67003 ttcaatataactgttaataataccacaacaggaattatattgaagaattccgattat 67062  
QY 2285 cctggccattgtcttgaaagacagcaagaaatctttgactgtatcagctctgc 2344  
|||||  
Db 67063 cctggccattgtcttgaaagacagcaagaaatctttgactgtatcagctctgc 67122  
QY 2345 aaggaacattgttcttccctgttccctgttccctaccattgaatcagattccgattta 2404  
|||||  
Db 67123 aaggaacattgttcttccctgttccctgttccctaccattgaatcagattccgattta 67182  
QY 2405 gtcaagaaagactcttcttggaacattcttagtaacctgaataattcttcttaattgcaga 2464  
|||||  
Db 67183 gtcaagaaagactcttcttggaacattcttagtaacctgaataattcttcttaattgcaga 67242  
QY 2465 agtggatgttcatgtggaagtatgagcttatttctccctcaactgtgtataatccttt 2524  
|||||  
Db 67243 agtggatgttcatgtggaagtatgagcttatttctccctcaactgtgtataatccttt 67300  
QY 2525 gaacttgctgttgcacaatgagcagaagggagagaga 2567  
|||||  
Db 67301 gaacttgctgttgcacaatgagcagaagggagagaga 67343

RESULT 4  
US-09-919-002-4478  
; Sequence 4478, Application US/09919002  
; GENERAL INFORMATION:  
; APPLICANT: Leshkowitz, Dena  
; APPLICANT: Liu, Jin  
; TITLE OF INVENTION: NOVEL CONFIGS OBTAINED FROM VARIOUS CDNA  
; FILE REFERENCE: 20411-752CON1  
; CURRENT APPLICATION NUMBER: US/09/919,002  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922  
; PRIOR FILING DATE: FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,341  
; PRIOR FILING DATE: FILING DATE: 1998-02-13  
; NUMBER OF SEQ ID NOS: 13203  
; SOFTWARE: FASTA/Seq for Windows Version 3.0  
; SEQ ID NO 4478  
; LENGTH: 1839  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-919-002-4478

Query Match 34.9%; Score 933.4; DB 5; Length 1839;  
Best Local Similarity 98.1%; Pred. No. 4.1e-182;  
Matches 976; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

QY 1574 ttgcatttttgccttagagctgataatgaacttccacaacatcctgtgagtgactttt 1633  
|||||  
Db 1 ttgcatttttgccttagagctgataatgaacttccacaacatcctgtgagtgactttt 60

QY 1634 ctctcgaattgaaacaaagtctatagcacaagaagctgca-tttttccacaaaaggaa 1692  
|||||  
Db 61 ctctcgaattgaaacaaagtctatagcacaagaagctgca-tttttccacaaaaggaa 120  
QY 1693 gacgtaacaaatggcacttcaaaccttctgggtcaaatatataatgatacagaagaatgttca 1752  
|||||  
Db 121 gatgttaacaaatggcacttcaaaccttctgggtcaaatatataatgatacagaagaatgttca 180  
QY 1753 aaatcataagtttaatgtgttttgaaaaaggccacaataataacttacttacttcttcaat 1812  
|||||  
Db 181 aaatcataagtttaatgtgttttgaaaaaggccacaataataacttacttacttcttcaat 240  
QY 1813 aatctgcaaatctctgcccgaatccgaaatctgaaatctgaaatgtactggttgaaacaaatt 1872  
|||||  
Db 241 aatctgcaaatctctgcccgaatccgaaatctgaaatctgaaatgtactggttgaaacaaatt 300  
QY 1873 tgtttgtgtgtagatataaatcatatccttattctcgggtgtgtttagattatgc 1932  
|||||  
Db 301 tgtttgtgtgtagatataaatcatatccttattctcgggtgtgtttagattatgc 360  
QY 1933 cagttccttataatttaaatcttctgtttatataatttgaaatgtccttataagatttct 1992  
|||||  
Db 361 cagttccttataatttaaatcttctgtttatataatttgaaatgtccttataagatttct 420  
QY 1993 taaattccttataagaacctataagaanaatcatatattaaatataacttaacagca 2052  
|||||  
Db 421 taaattccttataagaacctataagaanaatcatatattaaatataacttaacagca 480  
QY 2053 aaagcatccaataagataaggttatgtccttatttcttccagctgatacgaatg 2112  
|||||  
Db 481 aaagcatccaataagataaggttatgtccttatttcttccagctgatacgaatg 540  
QY 2113 aacacagtggttggaattcttgaagggaagtgaatgaatataattatctcagtggaact 2172  
|||||  
Db 541 aacacagtggttggaattcttgaagggaagtgaatgaatataattatctcagtggaact 600  
QY 2173 ttccatttaccacacttaccatatttggttccctgaggtatatacactaaattccagat 2232  
|||||  
Db 601 ttccatttaccacacttaccatatttggttccctgaggtatatacactaaattccagat 660  
QY 2233 attactgttaaatatacacaacagaagcaattatttgaaagatccgatttactccat 2292  
|||||  
Db 661 attactgttaaatatacacaacagaagcaattatttgaaagatccgatttactccat 720  
QY 2293 tgccttgaaaagcagcaggaacgaatcttgaactgtatcagctctgcagagcact 2352  
|||||  
Db 721 tgccttgaaaagcagcaggaacgaatcttgaactgtatcagctctgcagagcact 780  
QY 2353 ttgtttcccttggctcttggttccctacccttggaaatcagattccgatttagtcagaa 2412  
|||||  
Db 781 ttgtttcccttggctcttggttccctacccttggaaatcagattccgatttagtcagaa 840  
QY 2413 gacttcttggaacattcttagtaacctgaatcttctttaaattcatgaatgtgatt 2472  
|||||  
Db 841 gacttcttggaacattcttagtaacctgaatcttctttaaattcatgaatgtgatt 900  
QY 2473 gatcatgaagaagtgtatgtttattcttccctcaactgtgaaatcatcatttgaaactgc 2532  
|||||  
Db 901 gatcatgaagaagtgtatgtttattcttccctcaactgtgaaatcatcatttgaaactgc 958  
QY 2533 tgtttgcaatatggcagccacaagaaggagagaga 2567  
|||||  
Db 959 tgtttgcaatatggcagccacaagaaggagagaga 993

RESULT 5  
US-10-158-057-38  
; Sequence 38, Application US/10158057  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PJ205C1

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; CURRENT APPLICATION NUMBER: US/10/158,057
; CURRENT FILING DATE: 2002-06-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (80)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (659)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (664)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (756)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-158-057-38
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Query Match      27.3%; Score 730.8; DB 7; Length 757;
Best Local Similarity 98.4%; Pred. No. 1.4e-140;
Matches 743; Conservative 3; Mismatches 8; Indels 1; Gaps 1;
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QY 100 gtgacttcctcgccgacgagccgctcgcctctcggagacatgtctgctgctggcgagact 159
DB 2 gtgacttcctcgccgacgagccgctcgcctcgtgagacatgtctgctgctggcgagact 61
QY 160 tggcgtgtgccacccgagcgtctgcgacgagcagcgagcagcgacgacgacgacccctc 219
DB 62 tctgtgtgccacccgagcgtctgcgacgagcagcgagcagcgacgacgacgacccctc 121
QY 220 tccagcgactggacccgacatggagagtggtgagacatcggcgagctcgacgaggggc 279
DB 122 tccagcgactggacccgacatggagagtggtgagacatcggcgagctcgacgaggggc 181
QY 280 tcaagacctgggacccctcctcggccagagacgcgcgagggaaatttctactactggag 339
DB 182 tcaagacctgggacccctcctcggccagagacgcgcgagggaaatttctactactggag 241
QY 340 atgtcaacaagaatggagagctgagatttgaagaattatgaagtaccccttaagaacacag 399
DB 242 atgtcaacaagaatggagagctgagatttgaagaattatgaagtaccccttaagaacacag 301
QY 400 agaagaagaatgaatgagatlttaagaaglttaagacaaataatgaatggag 459
DB 302 agaagaagaatgaatgagatlttaagaaglttaagacaaataatgaatggag 361
QY 460 ctctcgaagaattgtccagctctccagacacctgggtctgacatcttctgaacaacagcag 519
DB 362 ctctcgaagaattgtccagctctccagacacctgggtctgacatcttctgaacaacagcag 421
QY 520 agttgattcttcaagaacattgattgattgattgattgattgattgattgattgattgatt 579
DB 422 agttgattcttcaagaacattgattgattgattgattgattgattgattgattgattgatt 481
QY 580 gagactacttctatttaactcctgtttacagacatltgaagaattatccglttctgaaac 639
DB 482 gagactacttctatttaactcctgtttacagacatltgaagaattatccglttctgaaac 541
QY 640 attctacaggaattgacatagggatagcttaactatccagaatgaattccacggaagacg 699
DB 542 attctacaggaattgacatagggatagcttaactatccagaatgaattccacggaagacg 601
QY 700 aaaaaaaatcccgagacaaatgtgtgagcagcttcttgacgaaggacatgtcgtgtcgtct 759
```

```
DB 602 aaaaaaaatcccgagacaaatgtgtgagcagcttcttgacgaaggacatgtcgtgtcgtc 661
QY 760 ctctgaacgaagcactgccccttctgacccgtctgaagaatcatgacagcttcagcttca 819
DB 662 ctctgaacgaagcactgccccttctgacccgtctgaagaatcatgacagcttcaagcttca 720
QY 820 aatcagaacaagaatgaacataattgtgtccttcca 854
DB 721 aatcagaacaagaatgaacataattgtgtccttcca 755
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```
RESULT 6
US-09-777-921A-120
; Sequence 120, Application US/09777921A
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS.
; FILE REFERENCE: AND USES THEREOF
; FILE REFERENCE: CL001103
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-777-921A-120
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Query Match      22.3%; Score 597.4; DB 5; Length 601;
Best Local Similarity 99.5%; Pred. No. 3.3e-113;
Matches 598; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 1539 atgaagaacaactttagagatgaacccagaagaatgatgtgtgatttttgcctttagcctgata 1598
DB 1 atgaagaacaactttagagatgaacccagaagaatgatgtgtgatttttgcctttagcctgata 60
QY 1599 atgaagaacttcaacaatctcgtgaatgacttttctcctcgaattgaaacaagctatg 1658
DB 61 atgaagaacttcaacaatctcgtgaatgacttttctcctcgaattgaaacaagctatg 120
QY 1659 gcaaaagaagctgacatcttcttcaacaagaaggagacgylaaacaatgctacttcaact 1718
DB 121 gcaaaagaagctgacatcttcttcaacaagaaggagacgylaaacaatgctacttcaact 180
QY 1719 ttgggactaattatataatgacacagaagaatgcttcaacatagattttaaagtgtttgaa 1778
DB 181 ttgggactaattatataatgacacagaagaatgcttcaacatagattttaaagtgtttgaa 240
QY 1779 aagggcacacaattataacttcttcttcaataatccctgcaaatctctgcctgaatc 1838
DB 241 aagggcacacaattataacttcttcttcaataatccctgcaaatctctgcctgaatc 300
QY 1839 cgaaatctgaaatgtactgcttgaacaaatltgtttgtgtttagagttataatc 1898
DB 301 ygaaatctgaaatgtactgcttgaacaaatltgtttgtgtttagagttataatc 360
QY 1899 attaatcttatttgcgggtgttttaagttatgacgagcttcttatttatttatttattctg 1958
DB 361 attaatcttatttgcgggtgttttaagttatgacgagcttcttatttatttatttattctg 420
QY 1959 ttctatatttgaatgtcttataagatttcttcaatttccotlatagaacatataa 2018
DB 421 ttctatatttgaatgtcttataagatttcttcaatttccotlatagaacatataa 480
QY 2019 gaaatcatltaatttaaaatataacacttcaagcaaaagcatccaaatlaagtaagagtt 2078
DB 481 gaaatcatltaatttaaaatataacacttcaagcaaaagcatccaaatlaagtaagagtt 540
QY 2079 atgtccttatttcttcttcaagctgaatacgaatgaacagatgtgtggaattctctgaagg 2138
```

Db 541 atgtccctattttcttcttcagctgaaacagacagctggcgaattctgaagg 600  
 Oy 2139 |  
 Db 601 a 601

```

RESULT 7
US-09-777-921A-121
: Sequence 121, Application US/09777921A
: GENERAL INFORMATION:
: APPLICANT: MERKULOV et al.
: TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: CL001103
: CURRENT APPLICATION NUMBER: US/09/777,921A
: CURRENT FILING DATE: 2002-02-07
: NUMBER OF SEQ. ID NOS: 126
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 121
: LENGTH: 601
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-777-921A-121

```

Query Match	22.3%	Score 597.4	DB 5	Length 601
Best Similarity	99.5%	Pred. No. 3.3e-113		
Matches 598	Conservative	1	Mismatches	2
			Indels	0
			Gaps	0

QY	1814	atccctgaaatccctccgcctggaatcccgaaatcgtgaagatgactcgtgtggaacaaattt	1873
Db	1	atccctgaaatccctccgcctggaatcccgaaatcgtgaagatgactcgtgtggaacaaattt	60
QY	1874	gtttctgtgtgagtgtaatacatcttaacttcttcgtggtgtgttacctatcttc	1933
Db	61	gtttctgtgtgagtgtaatacatcttaacttcttcgtggtgtgttacctatcttc	120
QY	1934	agttctcttatatttaattctctgtttatataatttgaatgctcttaagattcttt	1993
Db	121	agttctcttatatttaattctctgtttatataatttgaatgctcttaagattcttt	180
QY	1994	aaatttccttatgaaaccccttaatgagaataatcatcatcttaataataaccttaagaa	2053
Db	181	aaatttccttatgaaaccccttaatgagaataatcatcatcttaataataaccttaagaa	240
QY	2054	aagatccaataatgaatagtggtgttgatgctctattttctcttcgaagcgaataagaaga	2113
Db	241	aagatccaataatgaatagtggtgttgatgctctattttctcttcgaagcgaataagaaga	300
QY	2114	acacagtggtggaattctcgaagggaagtgaatgaatataatttatctcagtgggcactt	2173
Db	301	rcacagtggtggaattctcgaagggaagtgaatgaatataatttatctcagtgggcactt	360
QY	2174	ttccattttacccgcttaccattatttggtttccctgagtgtaacctaattttcaagata	2233
Db	361	ttccattttacccgcttaccattatttggtttccctgagtgtaacctaattttcaagata	420
QY	2234	ttactgttcaatataccaacaagaagcaatttttggaagaatcccggttaaccgcacat	2293
Db	421	ttactgttcaatataccaacaagaagcaatttttggaagaatcccggttaaccgcacat	480
QY	2294	gctttgaaaagcagcagaagaacgaaatttttgaactgtatcagcttctcgagaacatc	2353
Db	481	gctttgaaaagcagcagaagaacgaaatttttgaactgtatcagcttctcgagaacatc	540
QY	2354	ttgttttcccttgctccttggtttcttccactcttgaatacagatccggtttgacaagaag	2413
Db	541	ttgttttcccttgctccttggtttcttccactcttgaatacagatccggttttgaacaagaag	600
QY	2414	a 2414	

RESULT 8  
US-10-152-661-454  
; Sequence 454, Application US/10152661

```

1  APPLICANT: Watson, James D.
2  APPLICANT: Strachan, Lorna
3  APPLICANT: Sleeman, Matthew
4  APPLICANT: Orntust, Rene
5  APPLICANT: Muriston, James G.
6  APPLICANT: Kumble, Krishanand D.
7  TITLE OF INVENTION: Compositions Isolated From Skin Cells
8  TITLE OF INVENTION: and Methods for Their Use
9  FILE REFERENCE: 11000.1011c5
10 CURRENT APPLICATION NUMBER: US/10/152,661
11 CURRENT FILING DATE: 2002-05-20
12 PRIOR APPLICATION NUMBER: 09/866,050
13 PRIOR FILING DATE: 2001-05-24
14 PRIOR APPLICATION NUMBER: 60/721,232
15 PRIOR FILING DATE: 2000-07-25
16 PRIOR APPLICATION NUMBER: 60/206,650
17 PRIOR FILING DATE: 2000-05-24
18 PRIOR APPLICATION NUMBER: 09/312,283
19 PRIOR FILING DATE: 1999-05-14
20 PRIOR APPLICATION NUMBER: PCT/NZ99/00051
21 PRIOR FILING DATE: 1999-04-29
22 PRIOR APPLICATION NUMBER: 09/188,930
23 PRIOR FILING DATE: 1998-11-09
24 PRIOR APPLICATION NUMBER: 09/069,726
25 PRIOR FILING DATE: 1998-04-29
26 NUMBER OF SEQ ID NOS: 725
27 SOFTWARE: FastSeq for Windows Version 4.0
28 SEQ ID NO 454
29 LENGTH: 1808
30 TYPE: DNA
31 ORGANISM: Mouse
32 US-10-152-661-454

```

Query Match	20.48;	Score 545.4;	DB 7;	Length 1808;
Best Local Similarity	64.98;	Pred. No. 2.2e-102;		
Matches 807; Conservative	0;	Mismatches 436;	Indels 0;	Gaps 0;

QY	316	agggagaaaatttctaactctgagatgccaagaatgggaagctgattggaagat	377
Db	208	agcagaaaattctgtcaagcagatgtacaaagagccttgatgycacattggaagt	267
QY	376	ttatgaagttactttaaagaccattagagaaaatggaattgctcttaaggtttagaca	433
Db	268	ttgtacattacccccaagatcatatgagaanaaacctgagagctgtgttcaagagctctgacaca	327
QY	436	aaaaataatgacgaaaatgaaatgagctctcaagaattgtccactctccagaacatggtc	499
Db	328	aaaagaatgatggtcgaatctgatctcaagtgatcattcagctccctctgagacctggtg	387
QY	496	tgaactattctgacaacaacagcagatgttatcttccaagaatgatgattgtatggacaa	555
Db	388	tcaagatctctcgaaacacgacgacgagaaagtattcttaagagatgtgataagaatgacaga	447
QY	556	tgaacagtgacttgtaagaatgtagagaaactctcttattaaccctggtacagaacttg	615
Db	448	tgaaccatcgacttgcgaacagatgtgagaggaacttaccacccctctgacacctgtgagaacatcc	507
QY	616	aggaaatattccgtttcttgcgaaaaattctcacaaggaattgacatagggagatgacttacta	675
Db	508	cggagatcatccctgtactggaaggaacctcgaagatcttcgatgtcgtgagagaatctgcag	567
QY	676	ttccagatgaattccaaggaagcagaaaaaaatcccgagacaattggttgagagcactttgg	735
	568	tcccaagatggttctacacagttcgaaagagggcagaaacgggagatgtgttggaagcaccctgtg	627

Qy	736	caggagggcattgctgctgctcctcgcgaacagacatgcctctggagcgtctcga	795
Db	628	caggagggcagggcgagcagcttccagacccctgcacatcccccctggagcaacatg	687
Qy	796	tcatgctgacaggttcacaggttcaaatccagacaaatgacataatctggtcttcac	855
Db	688	tgccatgcaagctccatgctcccgacgacacaaatgctacgtcaggtgaggttccac	747
Qy	856	agatggtgaaagagggagctaccgcgtcttgagggggaatgtaataaacgtccac	915
Db	748	atagatctcgaggaaggggagccaaagctcatctcgggggcaagggcatcaatgtcc	807
Qy	916	aaatgctctcgaacagcagcttcaatctccggcatatgaacagtaacagaaagtact	975
Db	808	aaatgccccgagctcgccatcaaatctcatatgcatatgagcaatgaaacggctgcg	867
Qy	976	ctgaagaagacaaaataatgagacatttgagagattcttcgttccatgctgag	1035
Db	868	gtatgtatcaggaagcgtatgagatccacgaaagagctttgacagctcctctgcgag	927
Qy	1036	caactgacagacacttataatcatcatgagatttgaaacacggcgctgtgagca	1095
Db	928	ccattgcacagatagcatctccacatggaagcttcttgaaagccccaatgccccgga	987
Qy	1096	aaactgagcagctactcgtgataatgatgtgtccagaagaatttggaaacatgaagct	1155
Db	988	aaacagagacagactccgcatctgagctgtgcagagagatcttggataaagggtg	1047
Qy	1156	tggagacttttaacaaagctatgctcccaatttatagtatcaatctatgacga	1215
Db	1048	tactgctcttcaaaagagctatccccaacatgctggtgatactccctatgctgca	1107
Qy	1216	tagaatctgtctgtatgaacctctgaagtcctatggtctgagatcaatttggaaaagt	1275
Db	1108	tcgacctagctgtctatgagacatgtgaaataaccgctccagcgctacgaaatga	1167
Qy	1276	ctgtaaacccttgatgctatggtgtctcgtggatgctggagctcttaccagacctgtgc	1335
Db	1168	gtgcagagccccgggtgtgtctcgtctccctgcgtgtgtactctccagtaacttggcc	1227
Qy	1336	agctgagcagataccatctggtcttggtgaaactcgtgacagctcaagctcagttag	1395
Db	1228	agctgagcagataccatctggtcttggtgaaactcgtgacagctcaagctcagttag	1287
Qy	1396	aaggttcccaagctgaatatagtgttgcctcttcgcagaaattatccaaagaaggaa	1455
Db	1288	aggcgacactgagttacatgacagctcttcaacaagaattctcgtgactggggg	1347
Qy	1456	taccagacttttcaagagatcatccacaaacttataagttgctcctgctgtfagca	1515
Db	1348	cccttggctctccacggggctggccccaacttcaatgaaagtatcccgctgtgagca	1407
Qy	1516	tcaatgctggttatgtaaatatgaaagcaactttagagt	1558
Db	1408	tcagctacgtgctctacgaaaaccttgaagatcaacccttggcgct	1450
RESULT 9			
US-09-312-283B-262			
: Sequence 262, Application US/09312283B			
GENERAL INFORMATION:			
: APPLICANT: Watson, James D.			
: APPLICANT: Strachan, Lorna			
: APPLICANT: Steeman, Matthew			
: APPLICANT: Orrust, Rene			
: APPLICANT: Murison, James G.			
: APPLICANT: Kumble, Krishanad D.			
: TITLE OF INVENTION: Compositions Isolated from Skin Cells			
: FILE REFERENCE: 11000.1011c2			
: CURRENT APPLICATION NUMBER: US/09/312,283B			
: CURRENT FILING DATE: 1999-05-14			

```

; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Mouse
US-09-312-283B-262

Query Match      20.4%   Score 545.4;   DB 5;   Length 1816;
Best Local Similarity 64.9%;   Pred. No. 2.2e102;
Matches 807; Conservative 0; Mismatches 436; Indels 0; Gaps 0;

```

[illegible]





```

1  APPLICANT: Grimaldi,Christopher J.
2  APPLICANT: Gurney,Austin L.
3  APPLICANT: Watanabe,Collin K.
4  APPLICANT: Wood,William I.
5  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
6  TITLE OF INVENTION: ACIDS ENCODING THE SAME
7  FILE REFERENCE: P3230R1C1
8  CURRENT APPLICATION NUMBER: US/10/063,502
9  CURRENT FILING DATE: 2002-05-01
10 Prior Application removed - See File Wrapper or Palm
11 NUMBER OF SEQ ID NOS: 1/0
12 SEQ ID NO 57
13 LENGTH: 3334
14 TYPE: DNA
15 ORGANISM: Homo Sapien
16 US-10-063-502-57

```

Query Match	20.3%;	Score 543.8;	DB 7;	Length 3334;
Best Local Similarity	64.8%;	Pred. No. 5.6e-102;		
Matches 806;	Conservative 0;	Mismatches 437;	Indels 0;	Gaps 0;

QY	316	aggagaaatattttactactctggaagtgtccaaacaaagatvgggaagctggaatttgaagaat	375
Db	215	agcagaaatattgtcaacagctggaataaggacaccttgatvgggaagatagacttgaagaat	274
QY	376	ttatgaagtaccttaaaagacatggaagaagaatgtaaattggcatttgaagtttgaca	435
Db	275	ttgtccattatctccaaagatcaatgagaagaacgtgaagctcgtgtgtttaagaatttggaca	334
QY	436	aaaataatgatygaaaaaattgagcttcaagaattgtccagctctccagacactggtgc	495
Db	335	aaaagaatgatygagcgcgcatgacgagcagagatcatgacgtccctcggcgacttggag	394
QY	496	tgactattctcgacaacaaacagaggttgattcttccaagcatgtatgtttgttggacaa	555
Db	395	tcaagatattctgcaacacagcagacagaaaaattcttaagaagcattgataaaaaagcgaca	454
QY	556	tgaacagtgaactgtgaatgaatgagagagactcttctttaactcctttacagacatg	615
Db	455	tgaacatcgaactgtgaaacgagtgagaaagacatccacctctccacccgttgaacacatcc	514
QY	616	aggaaatatccgtttcttgcgaacaacattatacaggaattggacataagggatagaacta	675
Db	515	cggagatcatcctactctgtagaagcatctccacgactcttgattgtgtgttgaatctcaacg	574
QY	676	ttccagatgaatttcaacgaaagcagaaaaaaacccgagcaatgtgtgagcgactttg	735
Db	575	tcccggaatgagatttcaacatgtagagaaagcagacggygagtgtgtgtgagacacccgtg	634
QY	736	caggaaagcatctgcgtgtctgtctctgcgaacaagacgcccccttggacacgtctgaa	795
Db	635	caggaaagtgtgggcaggggcgttatccagaacactgcgacgcccccttgcacagcctcaag	694
QY	796	tcatgatgtcaggttcaacggttcaaaaatcagacaacaaatgaacatatitgtgtcttgac	855
Db	695	tgctcatgtcaggttcatgtccctcccgacagacaacacatgycatcgttgtgtgttcacac	754
QY	856	agatggttaaaagaagagagatccgctcgtcgttcttggaggggaaatggttcaaacgtcatca	915
Db	755	agatgatttcgaaagaagagacacaggttcaactctgtgcggygcacatggtacatcaacgtctca	814
QY	916	aaatgtctccctgagacagctgttaaatcttgcgcatatgaagaatgaagaagaatgtaacta	975
Db	815	aaatgtcccccgaaatcagacatcaaatcacaatgcacatgacctatgagaagaatcagcgccttgg	874
QY	976	ctgaagaagagcaaaaaaataagaaacatttggagagatatattctgttccatgcttggag	1035
Db	875	gtatgtaccagagagactctgagattcaacgagagccttcttggcaggtgtccttggcaagg	934
QY	1036	caactgtcacgaactttatatatccaatgagaggttatgaaaccagcgtgctgtatgca	1095
	935	ccatctgcacaaagacagcatcttaccacaatggagaggttcccttaagaacccggatgtggcgtcgga	994

QY	1096	aaactgagcgaactactcgtggaatatatgatgtgtgccagaagaattttgaaacatgaagct	11555
Db	995	agacagcgccagtaactacgtacggaatgtctgtgacatcgccgagagagatccctcggccagaagagggg	10544
QY	1156	tggagagcttttacaagaagcattgtcccaatttatatgaatcatcaccttatgagca	12151
Db	1055	tggccgctcttacaagaagcattgtgtcccaactatgtcgtgcatcatccctctgtccggca	11144
QY	1216	tagatctgtcgtgtatgatagctctctgaagtcactattgtcgtgataatttgcanaaagat	12757
Db	1115	tcgacctgtgcagcttaacgaagcactcaagaatgtcctgtcgtcagcacatgacatgagaca	11744
QY	1276	ctgtaaacccctggagctcatgtgtgtgtgttgagcgggtgctcatcacaacactgtgtc	13355
Db	1175	gctgcgagaccccgagctgttctgtgtgtccctgtgctcgtgtgaccaatgtccagtaactgtgtcc	12344
QY	1336	agctgcccagctacccaattgtgccttctgtgtgagaactcgtgacatgagctcaagcactgttag	13959
Db	1235	agctgtgcagctacccctctgccttagtcaagcccgagtcgaaggcgaagctctatgt	12944
QY	1336	aaggttcccacacgtgaatatgtgttgagctctcttcgcacgaattatttccaaagaagaa	14555
Db	1295	agggtgctcccgaaagtgcacattgacagacgtccttccaataatcctcgtgcgacaggagggg	13544
QY	1456	taccagagacttaagaagagcatcaaccaacttaagaagtgtccctctgtgagca	15151
Db	1355	ccttcgagctgttaagaagggtcgtgcccccacactcatatgaagtcatcccaagctgtgagca	14144
QY	1516	tcaagttatgtgtttatgtaaatatgaagcaaatcttagagat	1558
Db	1415	tcaagtaagtgtgtctacgaaacactgaagaatcaccctctgggcgt	1457

```

RESULT 13
US-10-063-510-57
; Sequence 57, Application us/10063510
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACID
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,510
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 57
; LENGTH: 3334
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-510-57

```

Query Match	20.3%;	Score 543.8;	DB 7;	Length 3334;
Best Local Similarity	64.8%;	Pred. No. 5.6e-102;		
Matches 806; Conservative	0;	Mismatches 437;	Indels 0;	Gaps 0

0y	316	agggagaaatttttctactctggaatgtaacaaagttggagctgatttgaagaat	375
Db	215	agcagaaattgttcaacgctggaatataagagccttggcagctacgacttgaagaat	274
0y	376	ttatgaagtaaccttaagacacatagaagaataatgtgcatttaagaagttgaca	435
Db	275	ttgtccattatctccaagatcatatagaagaagcctgaagcctgtttttaaattttgac	334



436 aaaaatgatgagaaaattgaggtctcagaaattgtccagctctccagacattggtc 495  
1111 11111111 1111 11 11 111111 11 1111  
335 aaaaagatgatgagcagcattgagcagcagagatcatgacgtcggtggtgag 394  
11 11 11111111 1111 1111 1111 1111 1111  
496 tgactattctgaacaacaagagttgattcttcaagcattgtgttgatggaca 555  
11 11 11111111 1111 1111 1111 1111 1111  
395 tcaagatctgaacagcagcagaaaattctcagagcatggaataaaacgacga 454  
11 11 11111111 1111 1111 1111 1111 1111  
556 tgacagtgcaggaatgagagagactactcttcaattcaatccgttaccagattg 615  
11 11 11111111 1111 1111 1111 1111 1111  
455 tgacctgcactggaacgaggtgagagactaccactctccaccccggtgaaaatcc 514  
11 11 11111111 1111 1111 1111 1111 1111  
616 aggaatataccgttcttgaaacattctacaggaattgacataggaggaatgacta 675  
11 11 1111 111111 1111 11 1111 1111 1111  
515 ccgagatcatccttacttgaagcatlccagatcttctgtgtggttgaaatcagg 574  
11 11 111111 1111 1111 1111 1111 1111  
676 ttccagatgaattcaggaagacgaaaataatccggaacaatggttgagggcagctt 735  
11 11 1111 1111 11 11 11 111111 11 1111  
575 tcccgatgatgacacagtgaggaagagacggggaatgtgtgagacacctgtgtg 634  
11 11 1111 1111 11 11 11 111111 11 1111  
736 caggagacattgctgtgtgtctctcgaacaagcactcccttggagccgtctga 795  
111111 11 11 11 1111 1111 1111 1111 1111  
635 caggaggttgggagcagggccgtatccagaaactcgacggcccccgtgacaggtcaa 694  
11 11 111111 11 11 1111 1111 1111 1111  
796 tcatgtacaggttccaggttccaaaatccagacaanaatgaacatattgtgtgtcag 855  
11 11111111 11 11 1111 1111 1111 1111 1111  
695 tgtcatgtacaggttccaggttcccccagacaacatgtgcatgtgtgtgtcactc 754  
11 11 111111 11 11 1111 1111 1111 1111  
856 agatgtgtaaagaaagagttatccgtctctgtgaggggaaatgtgtacaaactata 915  
111111 11111111 11 11 11 1111 1111 1111 1111  
755 agatgtatcgaagaagagggccaggttccatctcgcggggcaattgcatcaaacgtcc 814  
111111 11111111 11 11 11 1111 1111 1111 1111  
916 aaattctctctgagaaagtgtttaaattctgtgacatagaaacgttacaagaattact 975  
111111 11 11 1111 1111 1111 1111 1111 1111  
815 aaattgccccagatcagcatcaaaattcatgtgacctatgagcagatcaacggcgtt 874  
11 11 111111 11 11 1111 1111 1111 1111  
976 ctgaagaaggaacaanaataagaaactttgagagatttattctgtgttccatgtgtg 1035  
11 11 11 1111 11 11 1111 11 11 1111 1111  
875 gtatgtacacagagactctgaagatccaagaggtctgtgcaagggtcttctgtcagg 934  
11 11 111111 11 11 1111 1111 1111 1111  
1036 caactgtcagagactttatatatccaatgtgagttatgaaaacagggcgtgtgtg 1095  
11 11 1111 11 11 11111111 1111 1111 1111 1111  
935 ccatgccccagacagacatccacaaatgaggtctctgagagacggagatggcgctg 994  
11 11 1111 11 11 11111111 1111 1111 1111 1111  
1096 aaactgtgagactctctgaaatataatgattgtgccaagaagatttgaacaatgaag 1155  
11 11 11111111 1111 11 1111 11 11 1111 1111  
995 agacagagcagactactcagaatgtgtgactgcgcagagagatcccgccagagagg 1054  
11 11 111111 11 11 1111 11 11 1111 1111  
1156 tggagagcttttaacaagaagctatgttccaaattatlaagttatcaactatgag 1215  
11 11 11 11111111 1111 11 1111 11 11 1111 1111  
1055 tggcgctcttatacaaaagctatgtctccaaacatgtctggtgcatatccctatg 1114  
11 11 111111 11 11 1111 11 11 1111 1111  
1216 tgaattctgtgtatgtgagctcttgaagtccctatgagtgagtaatttggcaaaag 1275  
11 11 1111 11 11 1111 1111 1111 1111 1111  
1115 tgaacctgtgagcttaagagagcgtcacaagaatgctgcgtgcagacactatgacgt 1174  
11 11 1111 11 11 1111 1111 1111 1111 1111  
1276 ctgtaaacctgtgagctatggtgtgtgagatgaggtgcgttccatatacagacatg 1335  
11 11 1111 11 11 1111 1111 11 11 1111 1111  
1175 ggcgcagaccccggt 1234  
11 11 1111 11 11 1111 11 11 1111 1111 1111  
1336 agctgtgcagctacccaattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1395  
11 11 1111 1111 1111 11 11 11 1111 1111 1111  
1235 agctgtgcagctacccaattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1294  
11 11 1111 1111 1111 11 11 11 1111 1111 1111  
1396 aaggttccccacagctgaatatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1455  
11 11 11 1111 1111 1111 1111 11 11 11 1111  
1295 agggcgctccggaggtgacacatgagcagctcttcaaacatatacctgagcagagg 1354  
11 11 1111 11 11 1111 1111 11 11 11 1111  
1456 taaccagacttcaagagcatcaccaccaacttcaatgaagtgtccctgtgtatgag 1515  
11 11 1111 11 11 1111 1111 1111 1111 1111  
1355 ccttcggctgtatcaggggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1414  
11 11 1111 11 11 1111 1111 1111 1111 1111  
1516 tcaattatgtgtttatgaaaatatgaagcaactttagagt 1558  
11 11 1111 11 11 1111 1111 1111 1111 1111

1415 tcaagctacgtgttactagagaactgaactgaatcaccctgtgtgtgt 1457  
1111 11 1111 11 11 1111 11 11 11 1111  
RESULT 14  
US-10-063-512-57  
; Sequence 57, Application US/10063512  
; GENERAL INFORMATION:  
; APPLICANT: Falton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William T.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,512  
; CURRENT FILING DATE: 2002-05-01  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 57  
; LENGTH: 3334  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; US-10-063-512-57  
Query Match 20.3%; Score 543.8; DB 7; Length 3334;  
Best Local Similarity 64.8%; Pred. No. 5,6e-102;  
Matches 806; Conservative 0; Mismatches 437; Indels 0; Gaps 0;  
316 aggaagaattttactactgtgagatgtcaacaagaatggaggtctgtgtgaagaat 375  
11 11111111 11111111 11 111111 1111 11 11111111  
215 agcaagaatttgaacagcttgagataaggaacttgaatgtgagcagcttgaagaat 274  
11 11 111111 11111111 11 111111 1111 11 11111111  
376 tatgaagtaacttaagaagccatgagaagaataatgaaatgtgcatltaagaattaga 435  
11 11 1111 11 11111111 1111 11 111111 11 1111  
275 tgtccattatctccaaagtcataagaaagactgtgaggtgtgtgtgtgtgtgtgtgt 334  
11 11 111111 11 111111 11 11 1111 11 1111  
436 aaaaatgaatggaataattgaggtctcagaatgttccagttctccagacattgtgtc 495  
1111 11111111 1111 11 11 1111 11 11 1111 1111  
335 aaaaagatgatgagcagctacgcgcaggaagatcatgacgtcgtgaggtgtgtgtg 394  
11 11 111111 1111 11 11 1111 11 11 1111 1111  
496 tgactattctgaaacaacagagagttgattcttcaagaagcatgtgagtgtgtgagaa 555  
11 11 111111 111111 1111 11 1111 11 11 1111 1111  
395 tcaagatctgaacagcagcaggaanaaaattccaaagacatgagtaaaaacgacaga 454  
11 11 111111 111111 1111 11 1111 11 11 1111 1111  
556 tgacatgagctggaatgaaatgagagagacttcttatttcaattcgttaccagacattg 615  
11 11 111111 11111111 1111 11 11 1111 11 11 1111  
455 tgacctgcactggaacgaggtgagagactaccacactctccaccccggtgaaaatcc 514  
11 11 111111 111111 1111 11 11 1111 11 11 1111  
616 aggaatataccgttcttgaaacattctcagaagatgtacataggaggaatgacta 675  
11 11 1111 111111 1111 11 1111 11 11 1111 1111  
515 ccgagatcatccttacttgaagcatlccagatcttctgtgtgtgtgtgtgtgtgtgtgt 574  
11 11 1111 1111 1111 11 11 11 1111 1111 1111  
676 ttccagatgaattcaggaagacgaaaataatccggaacaatggttgagggcagctt 735  
11 11 1111 1111 11 11 11 111111 11 1111  
575 tcccgatgatgacacagtgaggaagagcagacgggagatgtgtgtgtgtgtgtgtgt 634  
11 11 1111 1111 11 11 11 111111 11 1111  
736 caggagacattgctgtgtgtctctcgaacaagcactcccttggagccgtctga 795  
111111 11 11 11 11 1111 1111 1111 1111 1111  
635 caggaggttgggagcagggcgtatccagaacctgcagcggcccccgtgacaggtcaa 694  
11 11 1111 11 11 1111 1111 11 11 11 1111  
796 tcatgtacaggttcaaggttcaaaaatcagaacaaatgaacatattgtgtgtgtgtgt 855  
11 111111 11 11 11 1111 11 11 11 111111 1111  
695 tgtcatgtaggttccatgtgtctccgagcagacaacatgtgtgtgtgtgtgtgtgt 754  
11 11 1111 11 11 1111 11 11 1111 1111 1111  
856 agatgtgtaaagaaagaggtatccgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 915  
1111 11 111111 11 11 11 1111 1111 1111 1111 1111



```

Db 755 agatgattcgaagaagggggccaggtcactctcggcgggcaatggtcatcaacgctccta 814
QY 916 aaatgctcctgaagacagctgtttaaattcttgggcataatgacaatgaagaagttaacta 975
Db 815 aaattgccccgaatcaagcatcaatlaaattgaatgagcagatcaagcgcttggtg 874
QY 976 ctgaaggaagacaaaataagaaactttgaagatttatatttctgttccatggtctgaag 1033
Db 875 gtagtgacaagaagaaactctgaagattcacaagaagggcttctgcaagggctcttgcaggg 934
QY 1036 caactgcacaagaactttatataatcatggaagttaaagaaacagagcgctgttagga 1095
Db 935 ccatacgcccaagacagacatactaccacaatgaaagtctctgaagaccggatagcgctcgga 994
QY 1096 aaactgggcagtaactctgaataatgatgatgtgtccagaagaacttttgaacaatgaagct 1155
Db 995 agacagcgcaagtactcaagaatgtgtgaactcgcgcaggaagatctctgcgcagaggggg 1054
QY 1156 tgggaagcttttaaaaggctatgtttcccaatttataggtatcataactttatgaagca 1211
Db 1055 tggcgcgcttctacaagaagctatgttcccaacatgtcgtgacatcaacccctatgcggca 1114
QY 1216 tagaatctgtcgtgtatgaagctcttgaagcctattggcgtcgtgaataatttgcanaaagatt 1275
Db 1115 tcgaactgtcagcttaagagaagcgtcaagaatgacctggtcgtcgacgactatgacgaga 1177
QY 1276 ctgtaaaccttggaagtcagtggtgtgtcgtggatcggtgacctatccagaacacctgtgtc 1335
Db 1175 ggcgcgaagcccggtgtgtgtgtgtcctcgtcgtcgtgtgacacatgtccagttactgtgccc 1234
QY 1336 agctggcgcaagctaccatttggcttgggtgaagactcgcatgcaaggtctcaagccatgttag 1395
Db 1235 agctggcgcaagctaccctctggcccttagtcagaccggatgcaaggcgcaagactctatgt 1294
QY 1396 aaggttcccccaagctaatatggtgtgcctcttcgcagaatattcttcaagaaggaa 1455
Db 1295 agggcgctccggaggtgacatcgtgacagctcctctcaaacatatccctggacccgggggg 1355
QY 1456 taccagaacttacaagagacatacaaccccaacttcaagaagtgtccctcgtgttagga 1515
Db 1355 ccttcggcgctgaacaggggcgctggcccccaacttcatgaagtcatccagctgtgagca 1414
QY 1516 tcagttatgtgtgttatgataaataatgaagcaactttagagct 1558
Db 1415 tcagctacgtgtgtctacgaagaacctgaagatcaccccttggcgct 1457

RESULT 15
US-10-063-513-57
; Sequence 57, Application US/10063513
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; PRIORITY FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 57
; LENGTH: 3334
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-063-513-57

```

[illegible]





Db 61 EKIFTTGVNKKDKGLDFEEFMKYLKDHKKMLAFKSLDKNNDKITEASEIVQSLOTIGL 120  
QY 121 TISEQOAEILLIOSIDVDGTMVDMNEMWDRDYFLFNPVTDIEEIIIRFKHSTGIDIGDSLTI 180  
Db 121 TISEQOAEILLIOSIDVDGTMVDMNEMWDRDYFLFNPVTDIEEIIIRFKHSTGIDIGDSLTI 180  
QY 181 PDETFEDEKSSQWMMROLIAGGIAGAVSRTSTAPLDRLKIIMQVHGSKSDKNNIFGGRQ 240  
Db 181 PDETFEDEKSSQWMMROLIAGGIAGAVSRTSTAPLDRLKIIMQVHGSKSDKNNIFGGRQ 240  
QY 241 MKKEGIRSLMNGNCTNVIKIPETAVKFWAYEYQKLLTEEGOKIGTFERFISGSMGA 300  
Db 241 MKKEGIRSLMNGNCTNVIKIPETAVKFWAYEYQKLLTEEGOKIGTFERFISGSMGA 300  
QY 301 TAQTFIYPMWVKTRILAVGKTQOYSIGIYDCAKKILKHEGLAFYGYVNPILGIIPYAGI 360  
Db 301 TAQTFIYPMWVKTRILAVGKTQOYSIGIYDCAKKILKHEGLAFYGYVNPILGIIPYAGI 360  
QY 361 DLAVYELKSYLDNFADKDSVNPGVWVLLGCGALSTGQOLASTYPLAVRTMQAOMLE 420  
Db 361 DLAVYELKSYLDNFADKDSVNPGVWVLLGCGALSTGQOLASTYPLAVRTMQAOMLE 420  
QY 421 GSPOLNMWGLFRITISKESIPGLYRGITPNEFKVLPAVGISVYVENMKOTLGVYOK 477  
Db 421 GSPOLNMWGLFRITISKESIPGLYRGITPNEFKVLPAVGISVYVENMKOTLGVYOK 477

RESULT 2  
PCT-US01-04098A-1739  
; Sequence 1739, Application PC/TUS0104098A  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-029  
; CURRENT APPLICATION NUMBER: PCT/US01/04098A  
; PRIOR APPLICATION NUMBER: Not Yet Assigned  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 09/728,422  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: 09/693,325  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/663,561  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: 09/654,936  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 09/620,325  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/598,075  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: 09/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 3960  
; SOFTWARE: Custom  
; SEQ ID NO 1739  
; LENGTH: 477  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US01-04098A-1739

Query Match 99.6%; Score 2471; DB 1; Length 477;  
Best Local Similarity 99.6%; Pred. No. 1.8e-213;  
Matches 475; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MRLWLDFALPTAACODAEQPTRYETLFCALDRNGDVVDIGELGRLNLGIPLGDAE 60  
Db 1 MRLWLDFALPTAACODAEQPTRYETLFCALDRNGDVVDIGELGRLNLGIPLGDAE 60  
QY 61 EKIFTTGVNKKDKGLDFEEFMKYLKDHKKMLAFKSLDKNNDKITEASEIVQSLOTIGL 120  
Db 61 EKIFTTGVNKKDKGLDFEEFMKYLKDHKKMLAFKSLDKNNDKITEASEIVQSLOTIGL 120

Db 61 EKIFTTGVNKKDKGLDFEEFMKYLKDHKKMLAFKSLDKNNDKITEASEIVQSLOTIGL 120  
QY 121 TISEQOAEILLIOSIDVDGTMVDMNEMWDRDYFLFNPVTDIEEIIIRFKHSTGIDIGDSLTI 180  
Db 121 TISEQOAEILLIOSIDVDGTMVDMNEMWDRDYFLFNPVTDIEEIIIRFKHSTGIDIGDSLTI 180  
QY 181 PDETFEDEKSSQWMMROLIAGGIAGAVSRTSTAPLDRLKIIMQVHGSKSDKNNIFGGRQ 240  
Db 181 PDETFEDEKSSQWMMROLIAGGIAGAVSRTSTAPLDRLKIIMQVHGSKSDKNNIFGGRQ 240  
QY 241 MKKEGIRSLMNGNCTNVIKIPETAVKFWAYEYQKLLTEEGOKIGTFERFISGSMGA 300  
Db 241 MKKEGIRSLMNGNCTNVIKIPETAVKFWAYEYQKLLTEEGOKIGTFERFISGSMGA 300  
QY 301 TAQTFIYPMWVKTRILAVGKTQOYSIGIYDCAKKILKHEGLAFYGYVNPILGIIPYAGI 360  
Db 301 TAQTFIYPMWVKTRILAVGKTQOYSIGIYDCAKKILKHEGLAFYGYVNPILGIIPYAGI 360  
QY 361 DLAVYELKSYLDNFADKDSVNPGVWVLLGCGALSTGQOLASTYPLAVRTMQAOMLE 420  
Db 361 DLAVYELKSYLDNFADKDSVNPGVWVLLGCGALSTGQOLASTYPLAVRTMQAOMLE 420  
QY 421 GSPOLNMWGLFRITISKESIPGLYRGITPNEFKVLPAVGISVYVENMKOTLGVYOK 477  
Db 421 GSPOLNMWGLFRITISKESIPGLYRGITPNEFKVLPAVGISVYVENMKOTLGVYOK 477

RESULT 3  
US-09-777-921-4  
; Sequence 4, Application US/09777921  
; GENERAL INFORMATION:  
; APPLICANT: MERKULOV et al  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; FILE REFERENCE: C1001103  
; CURRENT APPLICATION NUMBER: US/09/777,921  
; CURRENT FILING DATE: 2001-07-02  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 475  
; TYPE: PRT  
; ORGANISM: Rabbit  
US-09-777-921-4

Query Match 95.6%; Score 2373; DB 21; Length 475;  
Best Local Similarity 95.2%; Pred. No. 1.3e-204;  
Matches 454; Conservative 12; Mismatches 9; Indels 2; Gaps 1;  
QY 1 MRLWLDFALPTAACODAEQPTRYETLFCALDRNGDVVDIGELGRLNLGIPLGDAE 60  
Db 1 MRLWLDFALPTAACODAEQPTRYETLFCALDRNGDVVDIGELGRLNLGIPLGDAE 60  
QY 61 EKIFTTGVNKKDKGLDFEEFMKYLKDHKKMLAFKSLDKNNDKITEASEIVQSLOTIGL 120  
Db 61 EKIFTTGVNKKDKGLDFEEFMKYLKDHKKMLAFKSLDKNNDKITEASEIVQSLOTIGL 120  
QY 121 TISEQOAEILLIOSIDVDGTMVDMNEMWDRDYFLFNPVTDIEEIIIRFKHSTGIDIGDSLTI 180  
Db 121 TISEQOAEILLIOSIDVDGTMVDMNEMWDRDYFLFNPVTDIEEIIIRFKHSTGIDIGDSLTI 180  
QY 181 PDETFEDEKSSQWMMROLIAGGIAGAVSRTSTAPLDRLKIIMQVHGSKSDKNNIFGGRQ 240  
Db 181 PDETFEDEKSSQWMMROLIAGGIAGAVSRTSTAPLDRLKIIMQVHGSKSDKNNIFGGRQ 240  
QY 241 MKKEGIRSLMNGNCTNVIKIPETAVKFWAYEYQKLLTEEGOKIGTFERFISGSMGA 300  
Db 241 MKKEGIRSLMNGNCTNVIKIPETAVKFWAYEYQKLLTEEGOKIGTFERFISGSMGA 300  
QY 301 TAQTFIYPMWVKTRILAVGKTQOYSIGIYDCAKKILKHEGLAFYGYVNPILGIIPYAGI 360  
Db 301 TAQTFIYPMWVKTRILAVGKTQOYSIGIYDCAKKILKHEGLAFYGYVNPILGIIPYAGI 360

Db 299 TAOTFIYMEVMTKRLAVGKTGOYSGIYDCAKKILKEGFGAFYKGYVNNLGIIPYAGI 358  
QY 361 DLAVYELLSYWLNDNFPAKDSVNPVWVLLGCGALSTCGOLASYPALVTRRMOAAMLE 420  
Db 359 DLAVYELLSHWLDNFPAKDSVNPVWVLLGCGALSTCGOLASYPALVTRRMOAAMLE 418  
QY 421 GSPOLNMVGLFRRIRISKEGIPGLRGITPNNFMKVLPAVGISYVYVENMKOTLGVYOK 477  
Db 419 GADQLNMVGLFRRIRISKEGIPGLRGITPNNFMKVLPAVGISYVYVENMKOTLGVYOK 475

RESULT 4  
PCT-US01-14827-10548  
; Sequence 10548, Application PC/TUS0114827  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-104  
; CURRENT APPLICATION NUMBER: PCT/US01/14827  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/577,408  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 16102  
; SOFTWARE: Custom  
; SEQ ID NO 10548  
; LENGTH: 470  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (385)..(408)  
; OTHER INFORMATION: MITOCHONDRIAL CARRIER PROTEIN SIGNATURE domain identified by  
; OTHER INFORMATION: EMATRLX, accession number PR00926F, p-value=7.750e-19, raw score  
; NAME/KEY: DOMAIN  
; LOCATION: (222)..(466)  
; OTHER INFORMATION: Mitochondrial carrier proteins domain identified by Pfam,  
; OTHER INFORMATION: accession name mito\_carr, E-value=7.2e-71, Pfam score of 245.8  
PCT-US01-14827-10548

Query Match 90.5%; Score 2246; DB 1; Length 470;  
Best Local Similarity 91.4%; Pred. No. 3,6e-193;  
Matches 436; Conservative 2; Mismatches 3; Indels 36; Gaps 1;

QY 1 MRLWLRDFALPTAACODAPRTYETLFQALDRNGDGVVDIGLQGLRNLGIPLODAE 60  
Db 30 MRLWLRDFALPTAACODAPRTYETLFQALDRNGDGVVDIGLQGLRNLGIPLODAE 89  
QY 61 EKIFTTGVDNKGKLDFFEEFMKYLDHEKKMKLAFKSLDKNNNGKLEASEIVQSLQTLG 120  
Db 90 EKIFTTGVDNKGKLDFFEEFMKYLDHEKKMKLAFKSLDKNNNGKLEASEIVQSLQTLG 149  
QY 121 TISEQOAEILLQSIDVGTMTVDMNEMRDYFLFNPVTIDIEIIRFKHSTGIDIGSLTI 180  
Db 150 TISEQOAEILLQSIDVGTMTVDMNEMRDYFLFNPVTIDIEIIRFKHSTGIDIGSLTI 209  
QY 181 PPEFTEDEKSSGQWRRLLAGIAGAVSTRTAPLDRLKIMOVHSGSKDKNNIFEGFRO 240  
Db 210 PPEFTEDEKSSGQWRRLLAGIAGAVSTRTAPLDRLKIMOVHSGSKDKNNIFEGFRO 269  
QY 241 MVKEGGIRSLMNGSTNVIKIAPETAVKFWAYEQYKKLTLEGOKIGTFERFISGMAGA 300  
Db 270 MVKEGGIRSLMNGSTNVIKIAPETAVKFWAYEQYKKLTLEGOKIGTFERFISGMAGA 303  
QY 301 TQOTFIYMEVMTKRLAVGKTGOYSGIYDCAKKILKEGFGAFYKGYVNNLGIIPYAGI 360  
Db 304 TQOTFIYMEVMTKRLAVGKTGOYSGIYDCAKKILKEGFGAFYKGYVNNLGIIPYAGI 353  
QY 361 DLAVYELLSYWLNDNFPAKDSVNPVWVLLGCGALSTCGOLASYPALVTRRMOAAMLE 420  
Db 354 DLAVYELLSYWLNDNFPAKDSVNPVWVLLGCGALSTCGOLASYPALVTRRMOAAMLE 413

QY 421 GSPOLNMVGLFRRIRISKEGIPGLRGITPNNFMKVLPAVGISYVYVENMKOTLGVYOK 477  
Db 414 GSPOLNMVGLFRRIRISKEGIPGLRGITPNNFMKVLPAVGISYVYVENMKOTLGVYOK 470

RESULT 5  
US-09-777-921-5  
; Sequence 5, Application US/09777921  
; GENERAL INFORMATION:  
; APPLICANT: MERKULOV et al  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL001103  
; CURRENT APPLICATION NUMBER: US/09/777,921  
; CURRENT FILING DATE: 2001-07-02  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Human  
US-09-777-921-5

Query Match 85.9%; Score 2132; DB 21; Length 410;  
Best Local Similarity 99.8%; Pred. No. 5.5e-183;  
Matches 409; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 FALPTAACODAEQPTRYETLFQALDRNGDGVVDIGLQGLRNLGIPLODAEKEKIFTTG 67  
Db 1 FALPTAACODAEQPTRYETLFQALDRNGDGVVDIGLQGLRNLGIPLODAEKEKIFTTG 60  
QY 68 DVNKGKLDFFEEFMKYLDHEKKMKLAFKSLDKNNNGKLEASEIVQSLQTLGTTISQQA 127  
Db 61 DVNKGKLDFFEEFMKYLDHEKKMKLAFKSLDKNNNGKLEASEIVQSLQTLGTTISQQA 120  
QY 128 ELIQLSIDVGTMTVDMNEMRDYFLFNPVTIDIEIIRFKHSTGIDIGSLTIIDETED 187  
Db 121 ELIQLSIDVGTMTVDMNEMRDYFLFNPVTIDIEIIRFKHSTGIDIGSLTIIDETED 180  
QY 188 EKSGQWRRLLAGIAGAVSTRTAPLDRLKIMOVHSGSKDKNNIFEGFROVYKGGI 247  
Db 181 EKSGQWRRLLAGIAGAVSTRTAPLDRLKIMOVHSGSKDKNNIFEGFROVYKGGI 240  
QY 248 RSLMNGSTNVIKIAPETAVKFWAYEQYKKLTLEGOKIGTFERFISGMAGATAQFTY 307  
Db 241 RSLMNGSTNVIKIAPETAVKFWAYEQYKKLTLEGOKIGTFERFISGMAGATAQFTY 300  
QY 308 PMEVMTKRLAVGKTGOYSGIYDCAKKILKEGFGAFYKGYVNNLGIIPYAGIDLAVYEL 367  
Db 301 PMEVMTKRLAVGKTGOYSGIYDCAKKILKEGFGAFYKGYVNNLGIIPYAGIDLAVYEL 360  
QY 368 LKSYWLNDNFPAKDSVNPVWVLLGCGALSTCGOLASYPALVTRRMOAQA 417  
Db 361 LKSYWLNDNFPAKDSVNPVWVLLGCGALSTCGOLASYPALVTRRMOAQA 410

RESULT 6  
US-09-777-921-6  
; Sequence 6, Application US/09777921  
; GENERAL INFORMATION:  
; APPLICANT: MERKULOV et al  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL001103  
; CURRENT APPLICATION NUMBER: US/09/777,921  
; CURRENT FILING DATE: 2001-07-02  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 342





PRIOR APPLICATION NUMBER:	US 60/088, 033
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	US 60/088, 033
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	US 60/088, 326
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	US 60/088, 167
PRIOR FILING DATE:	1988-06-05
PRIOR APPLICATION NUMBER:	US 60/088, 202
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	US 60/088, 212
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	US 60/088, 217
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	US 60/088, 655
PRIOR FILING DATE:	1998-06-09
PRIOR APPLICATION NUMBER:	US 60/088, 722
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	US 60/088, 730
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	US 60/088, 734
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PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	US 60/089, 653
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	US 60/089, 801
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	US 60/089, 907

[illegible]



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; PRIOR APPLICATION NUMBER: US 60/091,626
; PRIOR FILING DATE: 1998-07-02
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; PRIOR APPLICATION NUMBER: US 60/092,472
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/093,339
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: US 60/094,651
; PRIOR FILING DATE: 1998-07-30

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Query Match      60.5%; Score 1501; DB 21; Length 469;
Best Local Similarity 65.8%; Pred. No. 5,8e-126;
Matches 275; Conservative 71; Mismatches 72; Indels 0; Gaps 0;

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QY 60 EKKIFITGVNNDGKIDFEFEFKYLLDKHKKKLAFLKSLDKNNDKIESEYISQITUG 119
    :||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 52 KOKIVAGKDLGGQIDFEFEFVHYLDHHEKRLVFKIILDKKNDGRIDAQEIQSLRDLG 111
QY 120 LTISEQOALILQSIDVDSTMTVDNMENRDFLEFNVDIEETIRPMKSTGIDIGSLT 179
    :||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 112 VKISEQAKIILKSMKNTMTIDNMENRDYHLHVEINPEIILYKWTSTIFDVENLT 171
QY 180 IPDEFTEDKSKGQWQKQLLAGIAGAVSRTSTAPLDRUKIMQVHGSKSDKNNIFGFR 239
    :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 172 VDFEVEERQGTGMWRHVLVAGGAGAVSRTCTAPLDRUKVLMQVHASRNNNGIYGFT 231
QY 240 ONWKEGGISLRNGSTNYIKIAPFAVKEFVAYEQYKILTEBGCKIGFEFRFISSMAG 299
    :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 232 QMIREGASLWRNGINVLKAPESATKFMAYEQIKRLVSGDQETLRHERVAGSLAG 291
QY 300 ATAQFIYMEYMKTRLAVKGTGYSGIYDCAKKILHGBLAFYGYVNLGIIPYAG 359
    :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 292 ALAQSSIVMEYLMKTRMALRKGTGYSGMLDCARRILARGVAFYGYVNMGIIPYAG 351
QY 360 IDLAVYELIKSTWLDNFAKDSVNPVGVVLLGCAUSSTCGQLASYPALVTRTMOQAML 419
    :||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 352 IDLAVYELIKNMVLGHYAVNSADPGVFLVLLAGTMSSTCGQLASYPALVTRTMOQASI 411
QY 420 EGGPOLNMVGLFRRIISKEIGIYRGITPNNPMKYLPAGISVYVYENMKOTLGYTQK 477
    :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 412 EGAPEVTMSLKHILRTGAGFGLRGALPNEMKYLPVAVISVYVENLKITLGVQSR 469

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RESULT 12  
US-09-941-992-289

; Sequence 289, Application US/09941992

; GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

```

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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C1
; CURRENT APPLICATION NUMBER: US/09/941,992
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/088738

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PRIOR APPLICATION NUMBER: 60/09247272	
PRIOR FILING DATE: 1998-07-09	

Query Match	60.5%;	Score 1501;	DB 23;	Length 469;
Best Local Similarity	65.8%;	Pred. No. 5.8e-126;		
Matches 275;	Conservative 71;	Mismatches 72;	Indels 0;	Gaps 0;

Qy	60	E E F T T G D V A N K D O C I D P E E R M K L X D H E K K M L A F S L D K N D K G I E A S I Y O S L O T L G	119
Dz	52	K Ö T I V O A D K D Q D O L D E E E V N H L O D H E K K L R V E F I Y I D K K N D G R I D A D E I M O S L D D	111
Qy	120	L T I E O O A E L L O S I D V D G T V T Y W N E M R D Y F L E N P A T D I E E I L R F M K H S T I D I G S L T	179
Dz	112	V K I S E O A E K L K S M D K N G M T I D M N E M R O Y H L H P E N I P E I L L Y K H S T I P D V G E N T	174
Qy	180	I P D E F T D E K K S G O W R O L L A G T A G A V S R T S T A P D I R L K I M O V H G S K S D K N I F G G F R	233
Dz	172	V P D E F T V E E R O T G M M H M I L V A G G A G A V S R C T A P D I R L V L M O V H A S R S N M G I Y G G T	231
Qy	240	O M V E G G I R S L M B R N G N I V L I A E T A V F K P M A Y O V K K L L T E B O C I G F E E R F T S G M G	299
Dz	232	O M I E G G A R S L M R N G N I V L I A E S I K F P A Y O I K R L V G S O D E T L R I H E R L A G S L A G	291
Qy	300	A T A O T F T Y P M E V M K T R L A V G T G O Y S G I Y D C A K K I L H E G I G A F K G Y V N L L G I I P Y A G	358
Dz	292	A I A O S S I Y P M E V L K T R M A L K R T G O Y S G I D C A R R I L L A R E G A A F K Y V N M L G I I P Y A G	351
Qy	360	I D L A V E L L K S Y L W D N F A K D S V N D G V N L L G C G A L S T C Q L A S Y P L A V R T R M O A O A M L	419
Dz	352	I D L A V E T L K N A M L O H Y A V N S A D P G V E V L L A C G M S S T C O L A S Y P L A V R T R M O A O A S I	411
Qy	420	E G S Q U L M V G L F R L I I S K E G I P G I R B I T P R E K V I P A V G I S Y V Y V N M Q I G A Y O K	477
Dz	412	E G A E I V M S S L F K I L I T E G A F G I Y R L A P F M K V I P A V S I Y V Y V N L K I T L I V O S R	469

RESULT 13  
US-09-989-279-289  
; Sequence 289, Application US/09989279  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerltisen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gueney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Tamas, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC56  
; CURRENT APPLICATION NUMBER: US/09/989,279  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
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; PRIOR FILING DATE: 1998-06-22  
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; PRIOR FILING DATE: 1998-06-23  
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2	PRIOR APPLICATION NUMBER: 60/090429
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4	PRIOR APPLICATION NUMBER: 60/090431
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17	PRIOR FILING DATE: 1998-06-24
18	PRIOR APPLICATION NUMBER: 60/090542
19	PRIOR FILING DATE: 1998-06-24
20	PRIOR APPLICATION NUMBER: 60/090557
21	PRIOR FILING DATE: 1998-06-24
22	PRIOR APPLICATION NUMBER: 60/090676
23	PRIOR FILING DATE: 1998-06-25
24	PRIOR APPLICATION NUMBER: 60/090678
25	PRIOR FILING DATE: 1998-06-25
26	PRIOR APPLICATION NUMBER: 60/090690
27	PRIOR FILING DATE: 1998-06-25
28	PRIOR APPLICATION NUMBER: 60/090694
29	PRIOR FILING DATE: 1998-06-25
30	PRIOR APPLICATION NUMBER: 60/090695
31	PRIOR FILING DATE: 1998-06-25
32	PRIOR APPLICATION NUMBER: 60/090696
33	PRIOR FILING DATE: 1998-06-25
34	PRIOR APPLICATION NUMBER: 60/090862
35	PRIOR FILING DATE: 1998-06-26
36	PRIOR APPLICATION NUMBER: 60/090863
37	PRIOR FILING DATE: 1998-06-26
38	PRIOR APPLICATION NUMBER: 60/091360
39	PRIOR FILING DATE: 1998-07-01
40	PRIOR APPLICATION NUMBER: 60/091478
41	PRIOR FILING DATE: 1998-07-02
42	PRIOR APPLICATION NUMBER: 60/091544
43	PRIOR FILING DATE: 1998-07-01
44	PRIOR APPLICATION NUMBER: 60/091519
45	PRIOR FILING DATE: 1998-07-02
46	PRIOR APPLICATION NUMBER: 60/091626
47	PRIOR FILING DATE: 1998-07-02
48	PRIOR APPLICATION NUMBER: 60/091633
49	PRIOR FILING DATE: 1998-07-02
50	PRIOR APPLICATION NUMBER: 60/091978
51	PRIOR FILING DATE: 1998-07-07
52	PRIOR APPLICATION NUMBER: 60/091982
53	PRIOR FILING DATE: 1998-07-07
54	PRIOR APPLICATION NUMBER: 60/092182
55	PRIOR FILING DATE: 1998-07-09
56	PRIOR APPLICATION NUMBER: 60/092472

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QY 240 QWKEGGJRSILMRGSGTVIITAPETLAKKMAAYOYKKILTBEOOKIGTERFISGGM 299
    ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 233 QMIRRGSGARSLMRGNGIIVLILAPSAIKEMAYOIKRLGSDOETLRHERLVAGSLAG 231
QY 300 ATAQTFIYPMEMYKRLRLAVGRTGQYSGIYDCAKKILKHEGIGAAYKGYVNNLGIIPYAG 359
    ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 292 ALAOSSTIYPMELTKRMLLRKTGQYSGMLDCARRILAREGVAAAYKGYVNNLGIIPYAG 351
QY 360 IDLAVYELLKSTYLDNFKADSVNPGVWVLLGCGALSTCGOLASYPLALVYTRMOAOAML 419
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 352 IDLAVYETLKNAMLOHYAVNSADPGVEVLLACGTSMSTCGOLASYPLALVYTRMOAASI 411
Db
QY 420 EGGPOLNMGVIFRRIISKEGIPGILYRGITPRFMVLAVNGISVYVYVNMKOTLGYNQK 477
    ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 412 ECAPVYVMSLSFKHLIRTEGAFGLYRGIAIPFMKVIIPAVSISVYVYVNNLKILITLGVOSR 469

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US-09-989-293A-289
Sequence 289, Application US/09989293A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan. L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Matanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P166
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609

```



Query Match	60.5%	Score 1501;	DB 23;	Length 469;
Best Local Similarity	65.8%;	Pred. No. 5.8e-126;		
Matches 275;	Conservative 71;	Mismatches 72;	Indels 0;	Gaps 0;

[illegible]

```

RESULT 15
US-09-989-721-289
; Sequence 289, Application US/09989721
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
; TITLE OR INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C5
; CURRENT APPLICATION NUMBER: US/09/989, 721
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12

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PRIOR APPLICATION NUMBER:	60/065311
PRIOR FILING DATE:	1997-11-13
PRIOR APPLICATION NUMBER:	60/066770
PRIOR FILING DATE:	1997-11-24
PRIOR APPLICATION NUMBER:	60/075945
PRIOR FILING DATE:	1998-02-25
PRIOR APPLICATION NUMBER:	60/078910
PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/083322
PRIOR FILING DATE:	1998-04-28
PRIOR APPLICATION NUMBER:	60/084600
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/087106
PRIOR FILING DATE:	1998-05-28
PRIOR APPLICATION NUMBER:	60/087607
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087609
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087755
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087822
PRIOR FILING DATE:	1998-06-03
PRIOR APPLICATION NUMBER:	60/088021
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088023
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088033
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088033
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088167
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088207
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088212
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088217
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088217
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088555
PRIOR FILING DATE:	1998-06-09
PRIOR APPLICATION NUMBER:	60/088734
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088735
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088742
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088810
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088822
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088825
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088855
PRIOR FILING DATE:	1998-06-11
PRIOR APPLICATION NUMBER:	60/088861
PRIOR FILING DATE:	1998-06-11
PRIOR APPLICATION NUMBER:	60/088876
PRIOR FILING DATE:	1998-06-11
PRIOR APPLICATION NUMBER:	60/089105
PRIOR FILING DATE:	1998-06-12
PRIOR APPLICATION NUMBER:	60/089444
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089512
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089514
PRIOR FILING DATE:	1998-06-16

[illegible]

Query Match	60.5%	Score 1501;	DB 23;	Length 469;
Best Local Similarity	65.8%	Pred. NO. 5.8e-126;		
Matches 275; Conservative	71;	Mismatches 72;	Indels 0;	Gaps 0;

Search completed: August 18, 2002, 09:27:03  
Job time: 657 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 18, 2002, 09:21:00 ; Search time 90.36 Seconds  
(without alignments)  
1245.435 Million cell updates/sec

Title: US-09-777-921A-2  
2481  
Perfect score: 1 MLRWLRDFAIPTAACDAEQ.....VGISVYVENMKQTGVTQK 477  
Sequence:

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 710927 seqs, 235927762 residues

Total number of hits satisfying chosen parameters: 710927

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/1/paa/PC7\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep:\*  
  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2481	100.0	477	5	US-09-777-921A-2 Sequence 2, Appl
2	2373	95.6	475	5	US-09-777-921A-4 Sequence 4, Appl
3	2373	95.6	475	5	US-09-791-537-130652 Sequence 130652,
4	2132	85.9	410	5	US-09-777-921A-5 Sequence 5, Appl
5	2132	85.9	411	5	US-09-791-537-131726 Sequence 131726,
6	2132	85.9	411	7	US-60-389-987-765 Sequence 765, App
7	1781	71.8	342	5	US-09-777-921A-6 Sequence 6, Appl
8	1501	60.5	469	5	US-09-991-150-289 Sequence 289, App
9	1501	60.5	469	6	US-10-063-502-58 Sequence 58, Appl
10	1501	60.5	469	6	US-10-063-510-58 Sequence 58, Appl
11	1501	60.5	469	6	US-10-063-512-58 Sequence 58, Appl
12	1501	60.5	469	6	US-10-063-513-58 Sequence 58, Appl
13	1501	60.5	469	6	US-10-063-514-58 Sequence 58, Appl
14	1501	60.5	469	6	US-10-063-515-58 Sequence 58, Appl
15	1501	60.5	469	6	US-10-063-516-58 Sequence 58, Appl
16	1501	60.5	469	6	US-10-063-517-58 Sequence 58, Appl
17	1501	60.5	469	6	US-10-063-518-58 Sequence 58, Appl
18	1501	60.5	469	6	US-10-063-519-58 Sequence 58, Appl
19	1501	60.5	469	6	US-10-063-520-58 Sequence 58, Appl
20	1501	60.5	469	6	US-10-063-521-58 Sequence 58, Appl
21	1501	60.5	469	6	US-10-063-522-58 Sequence 58, Appl
22	1501	60.5	469	6	US-10-063-523-58 Sequence 58, Appl
23	1501	60.5	469	6	US-10-063-524-58 Sequence 58, Appl
24	1501	60.5	469	6	US-10-063-525-58 Sequence 58, Appl
25	1501	60.5	469	6	US-10-063-526-58 Sequence 58, Appl
26	1501	60.5	469	6	US-10-063-528-58 Sequence 58, Appl

27	1501	60.5	469	6	US-10-063-529-58	Sequence 58, Appl
28	1501	60.5	469	6	US-10-063-530-58	Sequence 58, Appl
29	1501	60.5	469	6	US-10-063-532-58	Sequence 58, Appl
30	1501	60.5	469	6	US-10-063-534-58	Sequence 58, Appl
31	1501	60.5	469	6	US-10-063-536-58	Sequence 58, Appl
32	1501	60.5	469	6	US-10-063-537-58	Sequence 58, Appl
33	1501	60.5	469	6	US-10-063-538-58	Sequence 58, Appl
34	1501	60.5	469	6	US-10-063-540-58	Sequence 58, Appl
35	1501	60.5	469	6	US-10-063-541-58	Sequence 58, Appl
36	1501	60.5	469	6	US-10-063-544-58	Sequence 58, Appl
37	1501	60.5	469	6	US-10-063-546-58	Sequence 58, Appl
38	1501	60.5	469	6	US-10-063-547-58	Sequence 58, Appl
39	1501	60.5	469	6	US-10-063-548-58	Sequence 58, Appl
40	1501	60.5	469	6	US-10-063-549-58	Sequence 58, Appl
41	1501	60.5	469	6	US-10-063-550-58	Sequence 58, Appl
42	1501	60.5	469	6	US-10-063-551-58	Sequence 58, Appl
43	1501	60.5	469	6	US-10-063-553-58	Sequence 58, Appl
44	1501	60.5	469	6	US-10-063-554-58	Sequence 58, Appl
45	1501	60.5	469	6	US-10-063-555-58	Sequence 58, Appl

ALIGNMENTS

```
RESULT 1
US-09-777-921A-2
; Sequence 2, Application US/09777921A
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: C1001103
; CURRENT APPLICATION NUMBER: US/09/777, 921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 477
; TYPE: PRT
; ORGANSIM: Homo sapiens
US-09-777-921A-2

Query Match      100.0%; Score 2481; DB 5; Length 477;
Best Local Similarity 100.0%; Pred. No. 7.8e-195;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLRWLRDFAIPTAACDAEQPTREYETLFOALDRGSDVDVIGELQELRNIGIPLAGDAE 60
        |||||||
Db      1 MLRWLRDFAIPTAACDAEQPTREYETLFOALDRGSDVDVIGELQELRNIGIPLAGDAE 60

QY      61 EKIFTTGVDVNRKDLDFEERPMKYLIKDEHKMKKLAFKSLDRNNDGKIBASEIVQSLOTGL 120
        |||||||
Db      61 EKIFTTGVDVNRKDLDFEERPMKYLIKDEHKMKKLAFKSLDRNNDGKIBASEIVQSLOTGL 120

QY      121 TISEQQAELLQSDIDVDGCTVTVDMNENRQDFLPRPVYDIEIRFMKHSIGIDGSLTI 180
        |||||||
Db      121 TISEQQAELLQSDIDVDGCTVTVDMNENRQDFLPRPVYDIEIRFMKHSIGIDGSLTI 180

QY      181 PDFTFDEKKSQGMWRRLLAGIAGAVSRPTAPLDRLKIMQVHGSKSRKMNIFGSGFRQ 240
        |||||||
Db      181 PDFTFDEKKSQGMWRRLLAGIAGAVSRPTAPLDRLKIMQVHGSKSRKMNIFGSGFRQ 240

QY      241 MKREGGIRSLMRNGTNGTVIKIAPETAVKFWAYEQYKRLTIEEGOKIGTFERFISGSNAGA 300
        |||||||
Db      241 MKREGGIRSLMRNGTNGTVIKIAPETAVKFWAYEQYKRLTIEEGOKIGTFERFISGSNAGA 300

QY      301 TAQTFIYPMVVMKTRIAVGTGQSGIYDCAKKTILKEGIGATPKYKGVVPLGLITIPAGI 360
        |||||||
Db      301 TAQTFIYPMVVMKTRIAVGTGQSGIYDCAKKTILKEGIGATPKYKGVVPLGLITIPAGI 360

QY      361 DLAVYELLKSYMDNFNAKDSVNPGVVVLTCGALSTFCQGLASYPALVTRRMQAQMLE 420
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|||||
Db 361 DLAVVELLSYWLDFNFAKSVNPGVAVLLGCGALSTSCQGLASYPALVTRTMOAAMLE 420
QY 421 GSPOLNMVGLFRRIISKEGIPGLYRGITPNNFMKVLPAVGISVYVENMKOTLGTVOK 477
Db 421 GSPOLNMVGLFRRIISKEGIPGLYRGITPNNFMKVLPAVGISVYVENMKOTLGTVOK 477

RESULT 2
US-09-777-921A-4
; Sequence 4, Application US/09777921A
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: C1001103
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-777-921A-4

Query Match 95.6%; Score 2373; DB 5; Length 475;
Best Local Similarity 95.2%; Pred. No. 5.5e-186;
Matches 454; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

QY 1 MLRWLRDFAALPTAACODAEQPTRYETLFOALDRNGDGVVDIGELGRLNGLPIGODAE 60
Db 1 MLRWLRGFVLPTAACOGAEPPTRYETLFOALDRNGDGVVDIRELGKSLGIPGODAE 60
QY 61 EKIFTTGVDNKGKLDPEEFMKYLLKDHEKKMKLAFKSLDKNDGKIEASEIVQSLOTGL 120
Db 61 EKIFTTGVDNKGKLDPEEFMKYLLKDHEKKMKLAFKSLDKNDGKIEASEIVQSLOTGL 120
QY 121 TISEQOAEELILOSIDVDGTMVDNMENRDYFLFNPTDIEELIRFMKSHSTGIDIGSLTI 180
Db 121 TISEQOAEELILOSIDGTMVDNMENRDYFLFNPDADIEELIRFMKSHSTGIDIGSLTI 180
QY 181 PDEFTDEKKSGQMMROLLAGIAGAVSRTSTAPLDRLKIMQVHSGSKDNINFGGFRQ 240
Db 181 PDEFTDEKKSGQMMROLLAGIAGAVSRTSTAPLDRLKIMQVHSGSKS - -NINFGGFRQ 238
QY 241 MKEGGIRSLMNGNTNVIKIPETAVKFWAYEQYKKLTTEGOKIGTFPERISGSMAGA 300
Db 239 MIKEGGVRSIMNGNTNVIKIPETAVKFWYEQYKKLTTEGOKIGTFPERISGSMAGA 298
QY 301 TAOFTYPMEVKTRILAVGKTQOYSGIYDCAKKILKHGELGAFYGYVNNLGIIPYAGI 360
Db 299 TAOFTYPMEVKTRILAVGKTQOYSGIYDCAKKILKYEFGAFYGYVNNLGIIPYAGI 358
QY 361 DLAVVELLSYWLDFNFAKSVNPGVAVLLGCGALSTSCQGLASYPALVTRTMOAAMLE 420
Db 359 DLAVVELLSYWLDFNFAKSVNPGVAVLLGCGALSTSCQGLASYPALVTRTMOAAMLE 418
QY 421 GSPOLNMVGLFRRIISKEGIPGLYRGITPNNFMKVLPAVGISVYVENMKOTLGTVOK 477
Db 419 GAPOLNMVGLFRRIISKEGIPGLYRGITPNNFMKVLPAVGISVYVENMKOTLGTVOK 475

RESULT 3
US-09-791-537-130652
; Sequence 5, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBR
```

```
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patencin version 3.0
; SEQ ID NO 130652
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-791-537-130652

Query Match 95.6%; Score 2373; DB 5; Length 475;
Best Local Similarity 95.2%; Pred. No. 5.5e-186;
Matches 454; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

QY 1 MLRWLRDFAALPTAACODAEQPTRYETLFOALDRNGDGVVDIGELGRLNGLPIGODAE 60
Db 1 MLRWLRGFVLPTAACOGAEPPTRYETLFOALDRNGDGVVDIRELGKSLGIPGODAE 60
QY 61 EKIFTTGVDNKGKLDPEEFMKYLLKDHEKKMKLAFKSLDKNDGKIEASEIVQSLOTGL 120
Db 61 EKIFTTGVDNKGKLDPEEFMKYLLKDHEKKMKLAFKSLDKNDGKIEASEIVQSLOTGL 120
QY 121 TISEQOAEELILOSIDVDGTMVDNMENRDYFLFNPTDIEELIRFMKSHSTGIDIGSLTI 180
Db 121 TISEQOAEELILOSIDADGTMVDNMENRDYFLFNPDADIEELIRFMKSHSTGIDIGSLTI 180
QY 181 PDEFTDEKKSGQMMROLLAGIAGAVSRTSTAPLDRLKIMQVHSGSKDNINFGGFRQ 240
Db 181 PDEFTDEKKSGQMMROLLAGIAGAVSRTSTAPLDRLKIMQVHSGSKS - -NINFGGFRQ 238
QY 241 MKEGGIRSLMNGNTNVIKIPETAVKFWAYEQYKKLTTEGOKIGTFPERISGSMAGA 300
Db 239 MIKEGGVRSIMNGNTNVIKIPETAVKFWYEQYKKLTTEGOKIGTFPERISGSMAGA 298
QY 301 TAOFTYPMEVKTRILAVGKTQOYSGIYDCAKKILKHGELGAFYGYVNNLGIIPYAGI 360
Db 299 TAOFTYPMEVKTRILAVGKTQOYSGIYDCAKKILKYEFGAFYGYVNNLGIIPYAGI 358
QY 361 DLAVVELLSYWLDFNFAKSVNPGVAVLLGCGALSTSCQGLASYPALVTRTMOAAMLE 420
Db 359 DLAVVELLSYWLDFNFAKSVNPGVAVLLGCGALSTSCQGLASYPALVTRTMOAAMLE 418
QY 421 GSPOLNMVGLFRRIISKEGIPGLYRGITPNNFMKVLPAVGISVYVENMKOTLGTVOK 477
Db 419 GAPOLNMVGLFRRIISKEGIPGLYRGITPNNFMKVLPAVGISVYVENMKOTLGTVOK 475

RESULT 4
US-09-777-921A-5
; Sequence 5, Application US/09777921A
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: C1001103
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-777-921A-5

Query Match 85.9%; Score 2132; DB 5; Length 410;
Best Local Similarity 99.8%; Pred. No. 2.5e-166;
Matches 409; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY      8  FALPTAACQDAEOPRTYETLFOALDRNGDGYVDIGELQEGRLNIGIPGQDAEEKIFTTG  67
Db      1  FVLPTAACQDAEOPRTYETLFOALDRNGDGYVDIGELQEGRLNIGIPGQDAEEKIFTTG  60
QY      68  DVNKDGKLDPEEFEMKYLLKDHEKKMKLAFKSLDKNNDKIEASEIVQSLOTGLTISEQQA  127
Db      61  DVNKGKLDPEEFEMKYLLKDHEKKMKLAFKSLDKNNDKIEASEIVQSLOTGLTISEQQA  120
QY      128  ELLIQSIDVGTMTYDWMEMRDYFLFNPVTDIIEETIRFWKSTGIDIDSLTIPEDEFED  187
Db      121  ELLIQSIDVGTMTYDWMEMRDYFLFNPVTDIIEETIRFWKSTGIDIDSLTIPEDEFED  180
QY      188  EKSSQMMRWOLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSSDKNNIFGCFROWWKEGGI  247
Db      181  EKSSQMMRWOLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSSDKNNIFGCFROWWKEGGI  240
QY      248  RSLMGNSTNYIKIAPETAFAVFWAYEQYKLLTEBGOKIGTEERFISGSMAGATAQETIY  307
Db      241  RSLMGNSTNYIKIAPETAFAVFWAYEQYKLLTEBGOKIGTEERFISGSMAGATAQETIY  300
QY      308  PMEYVKTKTLAVGKQGYSGIYDCAKKILKHGSLAFYGYGYPNLLGITPYAGIDLAVEL  367
Db      301  PMEYVKTKTLAVGKQGYSGIYDCAKKILKHGSLAFYGYGYPNLLGITPYAGIDLAVEL  360
QY      368  LKSYWLDPFAKDSVNPGYMVLGCGALSTGQGLASYPALAVRTMQQA  417
Db      361  LKSYWLDPFAKDSVNPGYMVLGCGALSTGQGLASYPALAVRTMQQA  410

RESULT 5
US-09-791-537-131726
; Sequence 131726, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Dede, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 131726
; LENGTH: 411
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-791-537-131726

Query Match      85.9%  Score 2132:  DB 5:  Length 411:
Best local similarity 99.8%:  Pred. No. 2.5e-166:
Matches 409:  Conservative 0:  Mismatches 1:  Indels 0:  Gaps 0:

QY      8  FALPTAACQDAEOPRTYETLFOALDRNGDGYVDIGELQEGRLNIGIPGQDAEEKIFTTG  67
Db      1  FVLPTAACQDAEOPRTYETLFOALDRNGDGYVDIGELQEGRLNIGIPGQDAEEKIFTTG  60
QY      68  DVNKDGKLDPEEFEMKYLLKDHEKKMKLAFKSLDKNNDKIEASEIVQSLOTGLTISEQQA  127
Db      61  DVNKGKLDPEEFEMKYLLKDHEKKMKLAFKSLDKNNDKIEASEIVQSLOTGLTISEQQA  120
QY      128  ELLIQSIDVGTMTYDWMEMRDYFLFNPVTDIIEETIRFWKSTGIDIDSLTIPEDEFED  187
Db      121  ELLIQSIDVGTMTYDWMEMRDYFLFNPVTDIIEETIRFWKSTGIDIDSLTIPEDEFED  180
QY      188  EKSSQMMRWOLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSSDKNNIFGCFROWWKEGGI  247
Db      181  EKSSQMMRWOLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSSDKNNIFGCFROWWKEGGI  240
QY      248  RSLMGNSTNYIKIAPETAFAVFWAYEQYKLLTEBGOKIGTEERFISGSMAGATAQETIY  307
Db      241  RSLMGNSTNYIKIAPETAFAVFWAYEQYKLLTEBGOKIGTEERFISGSMAGATAQETIY  300
QY      308  PMEYVKTKTLAVGKQGYSGIYDCAKKILKHGSLAFYGYGYPNLLGITPYAGIDLAVEL  367
Db      301  PMEYVKTKTLAVGKQGYSGIYDCAKKILKHGSLAFYGYGYPNLLGITPYAGIDLAVEL  360
QY      368  LKSYWLDPFAKDSVNPGYMVLGCGALSTGQGLASYPALAVRTMQQA  417
Db      361  LKSYWLDPFAKDSVNPGYMVLGCGALSTGQGLASYPALAVRTMQQA  410

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Db      241 RSLMGNGNTVIKIAPEIAVKKFMAEYQYKKLLTEBQCKIGTEFERFISSGMAQATQOTFIY 300
QY      308 PWEVVKTRILAVGKTGOYSGIYDCAKKILKHEGLGAFYKGYVNNLGIIPYAGIDLAVEL 367
      |||||||
Db      301 PWEVVKTRILAVGKTGOYSGIYDCAKKILKHEGLGAFYKGYVNNLGIIPYAGIDLAVEL 360
QY      368 LKSYWLDNFAKDSVNPQVWVLLGGCALSTCGQLASYPALAVRTTRMQQA 417
      |||||||
Db      361 LKSYWLDNFAKDSVNPQVWVLLGGCALSTCGQLASYPALAVRTTRMQQA 410

RESULT 6
US-60-389-987-765
; Sequence 765, Application US/60389987
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Colin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465P2
; CURRENT APPLICATION NUMBER: US/60/389,987
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 3025
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 765
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-389-987-765

Query Match      85.9%; Score 2132; DB 7; Length 411;
Best Local Similarity 99.8%; Pred. No. 2.5e-166;
Matches 409; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 FALPAPACODAEQPTRYEFLFQALDRNGGVVDIGELQGLNLGIPIGQDAEERKIFTTG 67
      |||||||
Db      1 FALPAPACODAEQPTRYEFLFQALDRNGGVVDIGELQGLNLGIPIGQDAEERKIFTTG 60
QY      68 DVNKGKGLDFFEEFMKYLLKDHEKKMKLAFKSLDKNNDGKIEASEIYQSLQTLGLTISEQA 127
      |||||||
Db      61 DVNKGKGLDFFEEFMKYLLKDHEKKMKLAFKSLDKNNDGKIEASEIYQSLQTLGLTISEQA 120
QY      128 ELIIQSIDVDGTMIVDWNEMWRDYFLFNPYTDIEEIIREFMKHSTGIDIGSLTIPEFTED 187
      |||||||
Db      121 ELIIQSIDVDGTMIVDWNEMWRDYFLFNPYTDIEEIIREFMKHSTGIDIGSLTIPEFTED 180
QY      188 EKKSQWWRQLLAGGIIAGAVSSTSTAPLDRLKIMQVHYSKSDKNNIFEGCFQNNKEGGI 247
      |||||||
Db      181 EKKSQWWRQLLAGGIIAGAVSSTSTAPLDRLKIMQVHYSKSDKNNIFEGCFQNNKEGGI 240
QY      248 RSLMGNGNTVIKIAPEIAVKKFMAEYQYKKLLTEBQCKIGTEFERFISSGMAQATQOTFIY 307
      |||||||
Db      241 RSLMGNGNTVIKIAPEIAVKKFMAEYQYKKLLTEBQCKIGTEFERFISSGMAQATQOTFIY 300
QY      308 PWEVVKTRILAVGKTGOYSGIYDCAKKILKHEGLGAFYKGYVNNLGIIPYAGIDLAVEL 367
      |||||||
Db      301 PWEVVKTRILAVGKTGOYSGIYDCAKKILKHEGLGAFYKGYVNNLGIIPYAGIDLAVEL 360
QY      368 LKSYWLDNFAKDSVNPQVWVLLGGCALSTCGQLASYPALAVRTTRMQQA 417
      |||||||
Db      361 LKSYWLDNFAKDSVNPQVWVLLGGCALSTCGQLASYPALAVRTTRMQQA 410

RESULT 7
US-09-777-921A-6
; Sequence 6, Application US/09777921A
; GENERAL INFORMATION:

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; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: AND USES THEREOF
; FILE REFERENCE: C1001103
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-777-921a-6
```

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Query Match          71.8%; Score 1781; DB 5; Length 342;
Best Local Similarity 100.0%; Pred. No. 1,1e-137;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 28 FQALDRNGDVVDIGELQGLRNLGIPLEGDAEKKIFTTGDVKNKDKLDFEEFMKYLKDH 87
DB 1 FQALDRNGDVVDIGELQGLRNLGIPLEGDAEKKIFTTGDVKNKDKLDFEEFMKYLKDH 60
QY 88 EKKMKLAKESLDKNDGKTEASEIYQSLQTLGLTISEQDAELTLOSIDYDGTMYVDANBW 147
DB 61 EKKMKLAKESLDKNDGKTEASEIYQSLQTLGLTISEQDAELTLOSIDYDGTMYVDANBW 120
QY 148 RYFLFNPPTDIEETIRFKHSTGIDGSLTIPDEFTEDEKSGQWMLLAGAGAV 207
DB 121 RYFLFNPPTDIEETIRFKHSTGIDGSLTIPDEFTEDEKSGQWMLLAGAGAV 180
QY 208 SRTSTAPLDRLKIMQVHSGSKDMKNIFGFRQWYKEGIRSLWNGNTNVIKIAPEYAV 267
DB 181 SRTSTAPLDRLKIMQVHSGSKDMKNIFGFRQWYKEGIRSLWNGNTNVIKIAPEYAV 240
QY 268 KFWAIEQYKKLLTEEGOKIGTFERFISGSMAGATQTFIYPHEVAKTRILAVKGTQYSGI 327
DB 241 KFWAIEQYKKLLTEEGOKIGTFERFISGSMAGATQTFIYPHEVAKTRILAVKGTQYSGI 300
QY 328 YDCAKKIKLHEGLGAFYKGYVNPNLGIIPYAGIDLAVYELLK 369
DB 301 YDCAKKIKLHEGLGAFYKGYVNPNLGIIPYAGIDLAVYELLK 342
```

```

RESULT 8
; Sequence 289, Application US/09991150
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrare, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
```

```

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C48
; CURRENT APPLICATION NUMBER: US/09/991,150
; CURRENT FILING DATE: 2001-11-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 532
; SEQ ID NO 289
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-991-150-289
```

```

Query Match          60.5%; Score 1501; DB 5; Length 469;
Best Local Similarity 65.8%; Pred. No. 1.5e-114;
Matches 275; Conservative 71; Mismatches 72; Indels 0; Gaps 0;
```

```

QY 60 EKITTTGDVKNKDKLDFEEFMKYLKDHKKKLAFLKSLDKNDGKTEASEIYQSLQTLG 119
DB 52 KQIYQAGDKLDGOLDDEEFVHYLDHKKRLVFKILDKKNDRIDAOEIMQSLRDLG 111
QY 120 LTIHQDAELTLOSIDVQGTMTDWNEMRDYFLNPVTDIEETIRFKHSTGIDGSLT 179
DB 112 VTIHQDAELTLOSIDVQGTMTDWNEMRDYFLNPVTDIEETIRFKHSTGIDGSLT 171
QY 180 IPDEFTEDEKSGQWMLLAGAGAVSRTSTAPLDRLKIMQVHSGSKDMKNIFGFR 239
DB 172 VPDEFTEDEKSGQWMLLAGAGAVSRTSTAPLDRLKIMQVHSGSKDMKNIFGFR 231
QY 240 QWVKGGRIRSLWNGNTNVIKIAPEYAVKFWAYEDYKKLLEEGOKIGTFERFISGMA 299
DB 232 QWVKGGRIRSLWNGNTNVIKIAPEYAVKFWAYEDYKKLLEEGOKIGTFERFISGMA 291
QY 300 ATAQTFIYPHEVAKTRILAVKGTQYSGIYDCAKKIKLHEGLGAFYKGYVNPNLGIIPYAG 359
DB 292 ATAQTFIYPHEVAKTRILAVKGTQYSGIYDCAKKIKLHEGLGAFYKGYVNPNLGIIPYAG 351
QY 360 IDLAVYELLKSLWYDNFAKDSVNPVNLGCGALSTGCGQLASYPALAVTRMQQAAML 419
DB 352 IDLAVYELLKSLWYDNFAKDSVNPVNLGCGALSTGCGQLASYPALAVTRMQQAAML 411
QY 420 EGSPLQNVGLFRRIISLEGIGLRTIPNFMKYLPRVGSIVYVYENMKOTLGYTOR 477
DB 412 EGSPLQNVGLFRRIISLEGIGLRTIPNFMKYLPRVGSIVYVYENMKOTLGYTOR 469
```

```

RESULT 9
; Sequence 58, Application US/10063502
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,502
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 58
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-063-502-58
```



```
Db 352 IDLAAYETLKNAMLOHYAVNSADPGVFLACGTMSSFCGOLASYPALVTRMQOASI 411
QY 420 EGSPLNNVGLFRRILISKEGIPGLRGITPNNMKVLPAVGISYVYVENMKOTLGVTOK 477
Db 412 EGAPVETWSLFEKHILRTREGAFGLRGILAPNFMKVIPAVSISSYVYENLKITLGVSOR 469

RESULT 12
US-10-063-513-58
; Sequence 58, Application US/10063513
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; PRIOR FILING DATE: 2002-05-01
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 58
; LENGTH: 469
; TYPE: PRP
; ORGANISM: Homo Sapien
US-10-063-513-58

Query Match 60.5%; Score 1501; DB 6; Length 469;
Best Local Similarity 65.8%; Pred. No. 1.5e-114;
Matches 275; Conservative 71; Mismatches 72; Indels 0; Gaps 0;

QY 60 EKIITTDVNVKDKLDEEFPMKYLKDEHKMKLAFKSLDKNNDKIEASEIVOSLQTLG 119
Db 52 KQIVQAGDKDLDDGLDDEEFVHYLDHEKKRLVFKILDKKNDGRIDAQEOIMOSLRDLG 111
QY 120 LTISSQOAEILQSDVDGTMVDMNEMRDYFLPNVDIEIIFKMKHSTGIDGSLT 179
Db 112 VKISQOAEKILKSMKDKGTMTIDNENRDYHLHPVENIPILLYMKHSTIFDGENLT 171
QY 180 IPDEETDEKSKGOMWROLLAGIGAVSRTSTAPLDRLKIMQVHSGSKDMNIEGGR 239
Db 172 VPDEETVEERQGMWRRHLVAGGAVSRTCTAPLDRLKIMQVHASNMMGIYGGFT 231
QY 240 QMVEKGIRSLMRNGNTVNIKIAPETAVKFMAYEQYKLLTEEGOKIGTFERFISGMAG 299
Db 232 QMIRGAGARSIMRGINGIVLKIAPESAIFKMAVEQIKRLVSGDQETLRHERLVAGSLAG 291
QY 300 ATAQFTIPMEVMTKRLAVGTGQYSGLYDCAKKILKEHGAGAFKGYVNNLGIITPAG 359
Db 292 AIAOSIIPMEVLTKRLMRLKRTGQYSGLMDCAIRILAREGVAAFKGYVNNLGIITPAG 351
QY 360 IDLAAYETLKNAMLOHYAVNSADPGVFLACGTMSSFCGOLASYPALVTRMQOAML 419
Db 352 IDLAAYETLKNAMLOHYAVNSADPGVFLACGTMSSFCGOLASYPALVTRMQOASI 411
QY 420 EGSPLNNVGLFRRILISKEGIPGLRGITPNNMKVLPAVGISYVYVENMKOTLGVTOK 477
Db 412 EGAPVETWSLFEKHILRTREGAFGLRGILAPNFMKVIPAVSISSYVYENLKITLGVSOR 469

RESULT 13
US-10-063-514-58
; Sequence 58, Application US/10063514
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
```

```
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,514
; PRIOR FILING DATE: 2002-05-01
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 58
; LENGTH: 469
; TYPE: PRP
; ORGANISM: Homo Sapien
US-10-063-514-58

Query Match 60.5%; Score 1501; DB 6; Length 469;
Best Local Similarity 65.8%; Pred. No. 1.5e-114;
Matches 275; Conservative 71; Mismatches 72; Indels 0; Gaps 0;

QY 60 EKIITTDVNVKDKLDEEFPMKYLKDEHKMKLAFKSLDKNNDKIEASEIVOSLQTLG 119
Db 52 KQIVQAGDKDLDDGLDDEEFVHYLDHEKKRLVFKILDKKNDGRIDAQEOIMOSLRDLG 111
QY 120 LTISSQOAEILQSDVDGTMVDMNEMRDYFLPNVDIEIIFKMKHSTGIDGSLT 179
Db 112 VKISQOAEKILKSMKDKGTMTIDNENRDYHLHPVENIPILLYMKHSTIFDGENLT 171
QY 180 IPDEETDEKSKGOMWROLLAGIGAVSRTSTAPLDRLKIMQVHSGSKDMNIEGGR 239
Db 172 VPDEETVEERQGMWRRHLVAGGAVSRTCTAPLDRLKIMQVHASNMMGIYGGFT 231
QY 240 QMVEKGIRSLMRNGNTVNIKIAPETAVKFMAYEQYKLLTEEGOKIGTFERFISGMAG 299
Db 232 QMIRGAGARSIMRGINGIVLKIAPESAIFKMAVEQIKRLVSGDQETLRHERLVAGSLAG 291
QY 300 ATAQFTIPMEVMTKRLAVGTGQYSGLYDCAKKILKEHGAGAFKGYVNNLGIITPAG 359
Db 292 AIAOSIIPMEVLTKRLMRLKRTGQYSGLMDCAIRILAREGVAAFKGYVNNLGIITPAG 351
QY 360 IDLAAYETLKNAMLOHYAVNSADPGVFLACGTMSSFCGOLASYPALVTRMQOAML 419
Db 352 IDLAAYETLKNAMLOHYAVNSADPGVFLACGTMSSFCGOLASYPALVTRMQOASI 411
QY 420 EGSPLNNVGLFRRILISKEGIPGLRGITPNNMKVLPAVGISYVYVENMKOTLGVTOK 477
Db 412 EGAPVETWSLFEKHILRTREGAFGLRGILAPNFMKVIPAVSISSYVYENLKITLGVSOR 469

RESULT 14
US-10-063-515-58
; Sequence 58, Application US/10063515
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,515
; CURRENT FILING DATE: 2002-05-01
```

;; Prior Application removed - See File Wrapper or Palm  
;; NUMBER OF SEQ ID NOS: 170  
;; SEQ ID NO 58  
;; LENGTH: 469  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien  
US-10-063-515-58

Query Match 60.5%; Score 1501; DB 6; Length 469;  
Best Local Similarity 65.8%; Pred. No. 1.5e-114;  
Matches 275; Conservative 71; Mismatches 72; Indels 0; Gaps 0;

```
QY 60 EEKIFTTGVNKKDKLDPEEFEMKYLKDHEKKMKLAFKSLDKNNNDGKTEASEIVOSLQTLG 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 52 KQKIVAGDKDLQDLQDLPEEFVHYLDHKKRLVFKILDKKNGRIDAQEIIMQSLRDLG 111
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 120 LITSEQOAEILLOSIDVDGTMVDNEMRDYFLFNPVTDIEEIRFMKHSSTGIDIGSLT 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 112 VKISEQOAEKILKSMKNGMTMTIDNEMWRDYLHLHPVENIPEIILYWKHSTIFDVGENLT 171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 180 IPDEFTEDEKSSGOWMROLLAGIAGAVSRTSTAPLDRLKIMQVHSGSKDNKNIIFGFR 239
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 172 VPDEFTEERKOTGMMHHLVAGGAGAVSKTCTAPLDRLKVLMOVHASRSNNMGIVGGFT 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 240 QMKKEGIRSILMRNGNTNVIKIAPEYAVKFWAYEQYKLLTEEGOKIGTFEERFTSGSMAG 299
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 232 QMIREGARSILMRNGINVLKIAPESAIKFMAYEQIKRLVSGDQETLRIHERLVAGSLAG 291
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 300 ATAQTFIYPMKVMTKRLAVGKTGOYSIGYDCAKKILKHEGLGAFYKGYVPMNLGITIPYAG 359
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 292 AIAQSSIYPMKVMTKRLAVGKTGOYSIGYDCAKKILKHEGLGAFYKGYVPMNLGITIPYAG 351
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 360 IDLAAYELLKSYWLDNFAKDSVNPVNLGCGALSTCGQLASTYPLALVTRMOQAAML 419
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 352 IDLAAYETTLKNAWLQHYAVNSADPGVFLLAGCTMSSTCGQLASTYPLALVTRMOQAASI 411
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 420 EGSPOLNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVAGISYVYENMKOTLIGVTK 477
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 412 EGAPETVMSLFLKHLTREGAFGLYRGLAPNFMKVIIPAVSISYVYENLKITLIGVQSR 469
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RESULT 15
US-10-063-516-58
;; Sequence 58, Application us/10063516
;; GENERAL INFORMATION:
;; APPLICANT: Baton, Dan L.
;; APPLICANT: Flivaroff, Ellen
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3230R1C1
;; CURRENT APPLICATION NUMBER: US/10/063,516
;; CURRENT FILING DATE: 2002-05-01
;; Prior Application removed - See File Wrapper or Palm
;; NUMBER OF SEQ ID NOS: 170
;; SEQ ID NO 58
;; LENGTH: 469
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-063-516-58
```

Query Match 60.5%; Score 1501; DB 6; Length 469;  
Best Local Similarity 65.8%; Pred. No. 1.5e-114;  
Matches 275; Conservative 71; Mismatches 72; Indels 0; Gaps 0;

```
QY 60 EEKIFTTGVNKKDKLDPEEFEMKYLKDHEKKMKLAFKSLDKNNNDGKTEASEIVOSLQTLG 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 52 KQKIVAGDKDLQDLQDLPEEFVHYLDHKKRLVFKILDKKNGRIDAQEIIMQSLRDLG 111
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 120 LITSEQOAEILLOSIDVDGTMVDNEMRDYFLFNPVTDIEEIRFMKHSSTGIDIGSLT 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 112 VKISEQOAEKILKSMKNGMTMTIDNEMWRDYLHLHPVENIPEIILYWKHSTIFDVGENLT 171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 180 IPDEFTEDEKSSGOWMROLLAGIAGAVSRTSTAPLDRLKIMQVHSGSKDNKNIIFGFR 239
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 172 VPDEFTEERKOTGMMHHLVAGGAGAVSKTCTAPLDRLKVLMOVHASRSNNMGIVGGFT 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 240 QMKKEGIRSILMRNGNTNVIKIAPEYAVKFWAYEQYKLLTEEGOKIGTFEERFTSGSMAG 299
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 232 QMIREGARSILMRNGINVLKIAPESAIKFMAYEQIKRLVSGDQETLRIHERLVAGSLAG 291
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 300 ATAQTFIYPMKVMTKRLAVGKTGOYSIGYDCAKKILKHEGLGAFYKGYVPMNLGITIPYAG 359
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 292 AIAQSSIYPMKVMTKRLAVGKTGOYSIGYDCAKKILKHEGLGAFYKGYVPMNLGITIPYAG 351
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 360 IDLAAYELLKSYWLDNFAKDSVNPVNLGCGALSTCGQLASTYPLALVTRMOQAAML 419
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 352 IDLAAYETTLKNAWLQHYAVNSADPGVFLLAGCTMSSTCGQLASTYPLALVTRMOQAASI 411
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 420 EGSPOLNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVAGISYVYENMKOTLIGVTK 477
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 412 EGAPETVMSLFLKHLTREGAFGLYRGLAPNFMKVIIPAVSISYVYENLKITLIGVQSR 469
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Search completed: August 18, 2002, 09:28:54
Job time: 474 sec
```





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 18, 2002, 03:02:13 ; Search time 3254.77 Seconds  
(without alignments)  
17186.048 Million cell updates/sec

Title: US-09-777-921a-1  
Perfect score: 2673  
Sequence: 1 ccgcaccccgagcgccgccc.....ataccatgcatgtctctg 2673

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: GenEmbl:\*  
2: gb\_ba:\*  
3: gb\_htg:\*  
4: gb\_in:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_of:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htgo\_inv:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
-----				

1	2261	84.6	3259	9	AF123303	AF123303 Homo sapi	
2	1389	52.0	3298	4	AF004161	AF004161 Oryctolagi	
C	3	1138.2	42.6	170026	2	AC013627	AC013627 Homo sapi
C	4	1136.6	42.5	183037	9	AL390036	AL390036 Human DNA
5	1126	42.1	159384	2	AL356110	AL356110 Homo sapi	
6	657.2	24.6	1089	10	BC022637	BC022637 Mus muscu	
7	545.4	20.4	2555	10	BC019978	BC019978 Mus muscu	
8	545.4	20.4	2576	10	BC022114	BC022114 Mus muscu	
9	543.8	20.3	3334	6	AX092326	AX092326 Sequence	
10	498	18.6	3712	9	AB067483	AB067483 Homo sapi	
11	495.8	18.5	2857	9	AK054901	AK054901 Homo sapi	
12	436	16.3	1929	6	AX338084	AX338084 Sequence	
13	403.2	15.1	1294	9	HS080056	AL050209 Homo sapi	
14	385.4	14.4	2757	9	BC005163	BC005163 Homo sapi	
15	332.2	12.4	578	6	AX340234	AX340234 Sequence	
C	16	318.4	11.9	159384	2	AL356110	AL356110 Homo sapi
C	17	318.4	11.9	188622	9	AL359258	AL359258 Human DNA
18	306.6	11.5	2089	9	BC001656	BC001656 Homo sapi	
19	215.6	8.1	175811	2	AC095336	AC095336 Rattus no	
20	187.4	7.0	1843	8	AY056219	AY056219 Arabidops	
21	179.6	6.7	27598	3	CEP55A11	272511 Caenorhabditi	
22	171.6	6.4	396	6	AX247315	AX247315 Sequence	
23	168.8	6.3	400	6	AX247311	AX247311 Sequence	
24	165.4	6.2	1473	10	BC004720	BC004720 Mus muscu	
C	25	160	6.0	175811	2	AC095336	AC095336 Rattus no
26	150	5.6	122100	2	AC007328	AC007328 Drosophil	
27	150	5.6	136451	2	AC020327	AC020327 Drosophil	
C	28	150	5.6	167342	3	AC093438	AC093438 Drosophil
C	29	150	5.6	265536	3	AE003541	AE003541 Drosophil
C	30	128	4.8	57246	8	AB010069	AB010069 Arabidops
C	31	125.8	4.7	178480	2	AL671921	AL671921 Mus muscu
C	32	124.2	4.6	116763	2	AT7211	AL163912 Arabidops
C	33	116.8	4.4	148906	2	AP003629	AP003629 Oryza sat
C	34	113.4	4.2	188622	9	AL359258	AL359258 Human DNA
C	35	98.6	3.7	53002	9	AL390038	AL390038 Human DNA
36	98.4	3.7	1397	8	AY062478	AY062478 Arabidops	
37	97	3.6	1030	8	AY063072	AY063072 Arabidops	
38	97	3.6	1414	8	AF370255	AF370255 Arabidops	
39	95	3.6	1233	4	BTGDCP	X66035 B. taurus mr	
40	89.2	3.3	1719	9	H0MMSCA	M31659 Human GT ml	
41	88.6	3.3	194056	9	AL590708	AL590708 Human DNA	
42	87	3.3	42143	2	AC011539	AC011539 Homo sapi	
C	43	87	3.3	141291	9	AC010503	AC010503 Homo sapi
C	44	87	3.3	152195	2	AC016331	AC016331 Homo sapi
45	86.6	3.2	68726	8	AB017063	AB017063 Arabidops	

## ALIGNMENTS

RESULT 1  
AF123303 LOCUS AF123303 3259 bp mRNA linear PRI 01-FEB-2000  
DEFINITION Homo sapiens calcium-binding transporter mRNA, partial cds.  
ACCESSION AF123303  
VERSION AF123303.1 GI:6841065  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 3259)

AUTHORS  
Biery, B. and Valle, D.  
Cloning and subcellular localization of a human calcium-binding  
transporter

JOURNAL  
Unpublished  
2 (bases 1 to 3259)

REFERENCE  
AUTHORS  
Biery, B. and Valle, D.  
Direct Submission

JOURNAL  
Submitted (25-JAN-1999) Pediatrics/Genetics, Johns Hopkins  
University, 725 N. Wolfe Street PCTB 803, Baltimore, MD 21205, USA

FEATURES  
1. 3259  
Location/Qualifiers





D	718	CTTTGGACAGATGATNAAGGAAGAGGAGTGCCTGCTGCTGAGAGGAATGGACAA	777
Q	908	gctcatcaaatctctctctgagacagctglttaattctgggcaltgaacagtacaaga	967
D	778	TGTCATTAAGATGGTCTCTGAGACGGCGGAAGTTCTGGGCTTATGACCACTACAGAA	837
Q	968	gttacttactgaagaagacaaaatcaggaacattgagagattatcttgcgttcac	1027
D	838	GTTCGTTACTGAGGAGGACAAAAATAGBACCCTTGGAGAGTTATTTCCGGTTCCAT	897
Q	1028	ggctggagcaactgagacagctctcttgaaatattgattgagcaagaattttaaaca	1147
D	898	GGCCGAGCCACCGCAGAGCTTATTTCCATGAGAGCTATGAAACCAAGCTGGC	957
Q	1088	tctagagcaactggagacagctctcttgaaatattgattgagcaagaattttaaaca	1147
D	958	TGTAGCAAACTGGACATATCTCTGGAAATATATGACTGGCCCAAGAAATTTGAAATA	1017
Q	1148	tgaaggtcttggagagcttttcaaaaggctatgtcccaatttcttgaatcataccta	1207
D	1018	TGAAGTTTGGAGCTTTTACAAAGGTATATGTTCCAAATTTATTTAGGATCATACCTTA	1077
Q	1208	tgcagagcatagactctgtctgtatgtagctcttgaagtcctattgtctgataatttgc	1267
D	1078	TGCAGGCAATAGACCTTGGTGATGAGCTCTTGAAATCCACTGGCTAGATTAATTTGC	1137
Q	1268	aaaagatctgtaaacccctgagfcaagtgcttgcggagatgagctgacttccagac	1327
D	1138	AAAAGACTGTGCAAACCTGGAGTTTGATTTGCTGGGGTGTGGGCTTATCCAGAC	1197
Q	1328	ctgtgtcagctgtgcagactacccattgtgcttgtgtgagaactgcgatgcagctaacg	1387
D	1198	CTGTGGCCAGTTGGGCACACTTCCCTTGGGTTGTGTGAGAACACGATCCAGCTCAAGC	1257
Q	1388	catgtctagaaggttcccaagagctgaaatggtgttgccctcttcgaggaattatccaa	1447
D	1258	CATGCTGGAAGGAGCCCCACAGCTGAACATGTGTGGGCTTTTAGAAGATTAATTTCCA	1317
Q	1448	agaagaataccaggaacttacaagagcatcaccccaacttcatagaagtgtccctgc	1507
D	1318	AGAAAGACTCCAGAGACTTTTACAGAGCATACCCCAACTTATGAAAGTCTCCCTGC	1377
Q	1508	tctagagctcagttatggtgttcttgaaatatgaagcaactcttagaggttaaccagaa	1567
D	1378	TGTAGGCACTACGCTACGGGCTATATGAAATATGAACAAACCTTAGGAGTAAACCAAA	1437
Q	1568	atgac - "gttcatttcttctttagcctgataatgaaacttcaacatctctggagt	1625
D	1438	GGATATAGGTTGAGGGCTGTGATCCAGCATTAATTTAGAAATCTTCAACATCTGTGAGA	1497
Q	1626	gaccttctctcctcgtgaattgaaacaagctacatgycaaaagaa-----	1667
D	1498	GAATGTTTCTCTTAATAATTTGCACAACTGTGGCAAAAAATCCAAACCAAAACAAA	1557
Q	1668	-----gcgcattctttcacaaaagggaagacgltaaacatgctcaactcaaa	1718
D	1558	AAGTGTACTTTTTTTTTTTTTTCCACCAAGGAGGAAACATATCAACATCACTTCAAA	1617
Q	1717	cttctgggctaaatataatgacagaaatgtlcaaaatcabagltttaaigtgtttg	1776
D	1618	CATTTCAGTTGAGTTTCCATACACAGAA - "TTCAAGGTCAATAGTTTAAATTAAGTTTG	1675
Q	1777	aaaagcacaacatctacttacttcttcttctaataac---tgcaatctgcgcct	1833
D	1676	GAAA -GCCACAAATTTGACGTATCTTCTGTATTAATCTCTTTGGCAATCTTAACCTT	1734
Q	1834	gaatccgaatctgaaatctgactgcgcttgaaacaaattgttttbggttaaggttat	1893
D	1735	TAGTCTCAATCTCAAAATGTATTTGGTGGACATAATTGTTTGTGTGTGAGAAATAT	1794
Q	1894	aaatcaatcaatcttattctgggtgtgttaagcttaagccagltccttataatcat	1953

Db	1795	A-----AACTTATATTGATTCAGTTTAAGAFAATATCCAGGTCTTTTATATTTGATG	1847
Oy	1954	tctgtt-----ttatatatttgatgcttcita	1984
Db	1848	TCTTTTAAAGCAAAATGATCAGAACCTCGATATACATATATTTTGAAATATCATATA	1907
Oy	1985	gattccttaaatcccttatagaaaccaataagaanaatcatlaccattiaaalalacc	2044
Db	1908	GACATCTTCGCACCTTTAATAATCATATAACGAANAATCACGTGACTTTAAATATGTT	1967
Oy	2045	ttacagcaaaagcatccaaaataaglataggglttagtgccttatttcttcagctgaa	2104
Db	1968	TT-----AAATATGTCCAAATAGATATGAGTTTTATATCTTCACCTTTCTTAAAGTGAA	2021
Oy	2105	tacgaatgaacaacagtggtggaatttcggaagggaagcgatgaataatlatatttcag	2164
Db	2022	CAGGAATCACAATAGTAGTGTGGAATTTATA--GAGAGAGATATAACTATTTATTTGCG	2079
Oy	2165	tggagcactttccatttaccacgttacatatttggttcctgaggtatcacctaatt	2224
Db	2080	TAGGACACTTTCACATTTGGC--TTGCACCTGTTATTTGATTTCTATATATTAATCACTGAT	2137
Oy	2225	ttcag 2229	
Db	2138	GTCAG 2142	
RESULT 3			
AC013627/c			
LOCUS			
DEFINITION	AC013627	170026 bp DNA linear HTG 12-MAR-2000	
		Homo sapiens clone RP11-11L4, WORKING DRAFT SEQUENCE, 4 unordered pieces.	
ACCESSION	AC013627		
VERSION	AC013627.3	GI:7107908	
KEYWORDS	HTG; HTGS_PHASEI; HTGS_DRAFT.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 170026)		
AUTHORS	Birren,B., Linton,L., Nusbaum,C. and Lander,E.		
TITLE	Homo sapiens, clone RP11-11L4		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 170026)		
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,		
	Baldwin,J., Barna,N., Beckery,R., Boguslavsky,L., Bouckgalter,B.,		
	Brown,A., Castle,A., Colangelo,M., Collins,S., Collamore,A.,		
	Cooke,P., DeRellano,K., Dewar,K., Domingo,M., Donelan,L., Doyle,M.,		
	Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,		
	Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heathford,A., Horton,L.,		
	Howland,J.C., Johnson,R., Jones,C., Kann,L., Kartas,A., Klein,J.,		
	Lemockky,J., Lien,C., Locke,K., Macdonald,P., Marquis,N.,		
	Mcwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,		
	Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,		
	Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,		
	Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,		
	Traflet,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,		
	Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome		
	Research, 320 Charles Street, Cambridge, MA 02141, USA		
	All repeats were identified using RepeatMasker:		
COMMENT	Smith, A.F.A. & Green, P. (1996-1997)		
	http://ftp.genome.washington.edu/RM/RepeatMasker.html		
	----- Genome Center		
	Center: Whitehead Institute/ MIT Center for Genome Research		
	Center code: WIBR		
	Web site: http://www-seq.wi.mit.edu		
	Contact: sequence.submissions@genome.wi.mit.edu		
	----- Project Information		
	Center project name: U3222		
	Center clone name: IL_L_4		

```
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 159084 bases at least Q40
Consensus quality: 167015 bases at least Q30
Consensus quality: 169021 bases at least Q20
Insert size: 172000; agarose-ftp
Insert size: 169726; sum-of-contrigs
Quality coverage: 5.3 in Q20 bases; agarose-ftp
Quality coverage: 5.4 in Q20 bases; sum-of-contrigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 30577: contig of 30577 bp in length
* 30578 30677: gap of 100 bp
* 30678 70700: contig of 40023 bp in length
* 70701 70800: gap of 100 bp
* 70801 119118: contig of 48318 bp in length
* 119119 119218: gap of 100 bp
* 119219 170026: contig of 50808 bp in length.
*
Location/Qualifiers
1..170026
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="RP11-11L4"
/clone_1lb="RPc1-11 Human Male BAC"
1..30577
/note="assembly_fragment"
vector_side:left
clone_end:SP6
vector_side:right
/note="assembly_fragment"
70801..119118
/note="assembly_fragment"
clone_end:T7
vector_side:right
119219..170026
/note="assembly_fragment"
BASE COUNT 50115 a 34183 c 34647 g 50780 t 301 others
ORIGIN

Query Match 42.6%; Score 1138.2; DB 2; Length 170026;
Best Local Similarity 98.7%; Pred. No. 8.1e-203;
Matches 1168; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 1385 agccatgtagaaggtcccccacagctgaatagtggtgctcttcgcagcaatatttc 1444
|||||
Db 128072 AGCCAGTGTAGAAGGTCCCAAGCTGAATATGTTGGCCTCTTCGACGAAATTTTC 128013

QY 1445 caaagaaggaataacagagcttacagagcaccaccaacttatgaagtgctccc 1504
|||||
Db 128012 CAAAGAAGGAATACAGAGCTTTACAGAGCAACCCCAAACTTCATGAAGGTGCTCCC 127953

QY 1505 tgcgtgaagcatcagttatggtttatgaataatgaacacacttaagagtaacca 1564
|||||
Db 127952 TGCGTGAAGCATCAGTTATGTTTATGAATAATGACCAACTTTAGAGTAACCCA 127893

QY 1565 gaaatgagtgcattcttgccttaagcctgaataatgaacttcaacaatctctggag 1624
|||||
Db 127892 GAAATGATGTGCAATTTTGTGCTTAGCCTGATAATTTGAACCTTCAACAATCTGAG 127833

QY 1625 tgactttctcctgaattgaacaagctatggcaaaagaagctgcattttttcac 1684
|||||
Db 127832 TGACTTTTCTCCTGCAATTTGAACAAGCTATGAGCAAAAAGAGCTGCATTTTTCACA 127773
```

```
QY 1685 aaaggaagaagcgttaacaatggtcactcaacttttgggtataatataatgatacaga 1744
|||||
Db 127772 AAAGGAAGAAGTGAACAATGCTCATTCAAACTTTTGGGCTAAATATATATGTAACAGA 127713

QY 1745 aatgttcaaaatcatgaatttaatggttttggaaagccacaatatacttatctt 1804
|||||
Db 127712 AATGTTCAAAATCATGATGTTTAAATGTTTGAAGGACACAAATATATCTTATCTT 127653

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QY 1925 gttatgcccagttcccttataatttaattctctgttttataataattgaaatgcttata 1984
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QY 1985 gatttcttaatttctcttataagaccatttaataagaataatcaatcaatataatacc 2044
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QY 2285 cctgccaattgcttgaagaacagcaggaacgaatttttgaactgtatcagctctgc 2344
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RESULT 4  
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LOCUS 181037 bp DNA linear PRI 06-SEP-2001  
DEFINITION Human DNA sequence from clone RP11-356M1 on chromosome 1, complete  
sequence.  
ACCESSION AL390036  
VERSION AL390036.17 GI:15523665  
KEYWORDS  
HMG.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.

REFERENCE 1 (bases 1 to 183037)  
AUTHORS Frankland, J.  
TITLE Direct Submission  
JOURNAL Submitted (06-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
requests: clonequest@sanger.ac.uk

## COMMENT

On Sep 7, 2001 this sequence version replaced gi:14456226.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all  
regions were either double-stranded or sequenced with an alternate  
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the  
assembly was confirmed by restriction digest. The following  
abbreviations are used to associate primary accession numbers given  
in the feature table with their source databases: Em: EMBL; SW: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information on the WORMPEP  
database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence  
was generated from part of bacterial clone contigs of human  
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping  
Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chrl  
RP11-356N1 is from the library RRC1-11.2 constructed by the group  
of Pieter de Jong. For further details see  
http://www.choi.org/bacpac/home.htm  
VECTOR: pBAC3.6  
This sequence is the entire insert of clone RP11-356N1 The true  
left end of clone RP11-483113 is at 170175 in this sequence. The  
true right end of clone RP11-320L5 is at 93687 in this sequence.

## FEATURES

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1. 183037

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/db\_xref="taxon:9606"

/chromosome="1"

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/clone\_lib="RRC1-11.2"

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(AL391235). Assembly confirmed by restriction digest."

79012..79019

/note="Sequence from overlapping clone RP11-320L5

(AL391235). Assembly confirmed by restriction digest."

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/note="Cpg island"

/evidence="not\_experimental"

BASE COUNT 55819 a 38180 c 35765 g 53273 t

ORIGIN

## Query Match

Best Local Similarity 42.5%; Score 1136.6; DB 9; Length 183037;

Matches 1167; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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1385 agccatgttaaaaggtcccccacagctgaatagtgtgctcttcgaagcaatatttc 1444

## Db

151015 AGCCATGTTAAAGGTTCCACACAGCTGAATATGTTGGCCCTTTTCACAGCAATATTTTC 150956

## Query

1445 caaagaagaataccagacttacagagcatcaaccccaactcatgaagtgctccc 1504

## Db

150955 CAAAGAAGAAATACCAGACTTTACAGAGGCTACACCCCAAACTTCATGAAGTCTCCC 150896

## Query

1505 tgcgtgaagcaacgltatgtgtttatgaataatgaagcaaaccttagagtaacca 1564

## Db

150895 TGCTGTAGGCAATGATGTATGTGTTATGAATAATGAAGCAAACTTTAGAGTAACCA 150836

## Query

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1625 tgacttttcctcgaatgtgaacaagctatgcaaaagaagctgatttttcaca 1684

Db 150775 TGACTTTTTCCTCGAATGTGAACAAGCTATGCAAAAGAGCTGCAATTTTTCACA 150716

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Db 150715 AAAGGAAGATGAGTGAACAATGTGCTCAAACTTTGGCTTAATATATGACACAGA 150656

1745 aatgttcaaatcgaattatgttttgaagaagccacaaatatacttactt 1804

Db 150655 AATGTTCAAAATCAGATTTTAATGTGTTGAAGAAGCCACACAAATATATCTTATCTT 150596

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Db 150475 GTTATGCGCAGTCTCTTATATTTTAATTTCTGTTTATATTTTGAATGTCTTTATA 150416

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2165 tgggaactttccatttccattacacactgtacacattattgttctcctgagttacactaa 2224

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2225 ttcaatatattcgttataattacacaacaagaagcaattatttgaagaatccgttat 2284

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2525 gaactgtcgttttgcataatggtcagcacaagaagggtgagaga 2567

Db 149877 GAACCTTGCTGTTTCAATATGAGGACGACAAAGTGAGAGATA 149835

RESULT 5

AL356110 159384 bp DNA linear HTG 15-MAY-2000

LOCUS AL356110 Homo sapiens chromosome 1 clone RP4-562N20 map p34.1-34.2, \*\*\*

DEFINITION SEQUENCING IN PROGRESS \*\*\*, 71 unordered pieces.

ACCESSION AL356110  
VERSION AL356110.1 GI:9213734  
KEYWORDS HTG: HTGS\_PHASE1.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 159384)  
REFERENCE Plumb, B.  
AUTHORS Direct Submission  
TITLE Submitted (14-MAY-2000) Sanger Centre, Hinxton, Cambridgeshire,  
JOURNAL CB10 15A, UK. E-mail enquiries: humquerry@sanger.ac.uk  
COMMENT On Jul 15, 2000 this sequence version replaced gi:7899229.  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquerry@sanger.ac.uk  
----- Project Information  
Center project name: d562N20  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: plasmid; L08752; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Consensus quality: 112062 bases at least Q40  
Consensus quality: 126393 bases at least Q20  
Consensus quality: 139133 bases at least Q20  
Insert size: 152384; sum-of-contigs  
Insert size: 119983; 3.4% error; agarose-fp  
Quality coverage: 1.75x in Q20 bases; sum-of-contigs Quality  
coverage: 2.22x in Q20 bases; agarose-fp  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 71 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
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3402 3501: contig of 3401 bp in length  
3502 5184: contig of 1683 bp in length  
5185 5284: gap of 100 bp  
5285 8399: contig of 3115 bp in length  
8400 8499: gap of 100 bp  
8500 9995: contig of 1496 bp in length  
9996 10095: gap of 100 bp  
10096 12393: contig of 2298 bp in length  
12394 14134: contig of 1641 bp in length  
14135 14234: gap of 100 bp  
14235 15647: contig of 1413 bp in length  
15648 15747: gap of 100 bp  
15748 17013: contig of 1266 bp in length  
17014 17113: gap of 100 bp  
17114 18234: contig of 1121 bp in length  
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20825 20924: gap of 100 bp  
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29469 30517: contig of 1049 bp in length  
30518 30617: gap of 100 bp  
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31805 31904: gap of 100 bp  
31905 35404: contig of 3500 bp in length  
35405 35504: gap of 100 bp

35505 40678: contig of 5174 bp in length  
40679 40778: gap of 100 bp  
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79969 81238: contig of 1270 bp in length  
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81339 83358: contig of 2020 bp in length  
83359 83458: gap of 100 bp  
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84639 86014: contig of 1376 bp in length  
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114987 115086: gap of 100 bp  
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116436 116535: gap of 100 bp  
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* 117711 118745: contig of 1035 bp in length
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* 118846 121003: contig of 2158 bp in length
* 121004 121103: gap of 100 bp
* 121104 123754: contig of 2651 bp in length
* 123755 123854: gap of 100 bp
* 123855 128129: contig of 4275 bp in length
* 128130 128229: gap of 100 bp
* 128230 132322: contig of 4093 bp in length
* 132323 132422: gap of 100 bp
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* 136177 136276: gap of 100 bp
* 136277 137352: contig of 1076 bp in length
* 137353 137452: gap of 100 bp
* 137453 139013: contig of 1561 bp in length
* 139014 139113: gap of 100 bp
* 139114 140439: contig of 1326 bp in length
* 140440 140539: gap of 100 bp
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* 144814 145850: contig of 1037 bp in length
* 145851 145950: gap of 100 bp
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* 157144 157243: gap of 100 bp
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QY 2546 ggcagccacaagaaggagagaga 2567
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Db 60348 GGCAGCACAAAAGGTGAGAGATA 60369

RESULT 6
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BC022637  
LOCUS BC022637 1089 bp mRNA linear ROD 04-FEB-2002  
DEFINITION Mus musculus, clone IMAGE:4208509, mRNA, partial cds.  
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VERSION BC022637.1 GI:18490465  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 1089)  
Strausberg, R.  
Direct Submission  
Submitted (01-FEB-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
DNA Sequencing by: Sequencing Group at the Stanford Human  
Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mdickpaxil.stanford.edu](mailto:mdickpaxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.  
Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>  
Series: IRAX Plate: 43 Row: h Column: 13  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Hexamer frequency OK  
analysis.  
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/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6"  
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YVENMKOTLGAOK"  
BASE COUNT 293 a 241 c 262 g 293 t  
ORIGIN  
Query Match 24.6%; Score 657.2; DB 10; Length 1089;  
Best Local Similarity 79.1%; Pred. No. 4,6e-113;  
Matches 851; Conservative 0; Mismatches 203; Indels 22; Gaps 5;

Db 121 TTAGGAGACCTTTGAGAGGTTTATCTGTGATCCATGGCTGAGCAACTGCTCAGACTTTT 180  
Qy 1053 atataaccaatggaggtttatgaacaaccagcctgctgtagcaaaactggcagctctc 1112  
Db 181 ATTACCCCATGGAGGTTTGAAGAACCCGGCTAGCTGATGCCAANAATGGACAAATCTCC 240  
Qy 1113 ggaatatatgatctgcacaaagaattttgaacaatgaagctctggagctttttcaaa 1172  
Db 241 GGAATATACGGTGTGTGCAAGAAAGATTTTGAACACAGAACGCTTTGGCGCTTTTACAA 300  
Qy 1173 ggcatactcccaattatagatcatcactatgacaggaatagatctctgctgtagt 1232  
Db 301 GGCTACATTCCTCCCAATTTACTAGGACATTCCTTACGACAGCATTTGCTGCTGTAC 360  
Qy 1233 gagctcttgaaagccattggctgagtaattttgcaaaagatctgtaaaccttgatc 1292  
Db 361 GAGCTTTTGAAGTCTTATGCTGGATTAACCTTGGCCAAAGACCTGGCTGCGGTG 420  
Qy 1293 atgtagtctgctggatgcggtgcttataccagcactgtgtcagctgagcactacca 1352  
Db 421 ATAGTCTCTGTGAGCTGTGAGAGCCCTATCCAGACCTGTGTGGCAGCTGGCAGCTACCC 480  
Qy 1353 ttgctcttgtagaactgcatacgatgcagctcaagcatgtagaaggttcccaagctg 1412  
Db 481 CTGGCTTTGGTGAAGTCTGCATGACAGCTCAAGCCAGGATAGAGAGCCCGCAGACTG 540  
Qy 1413 aatatgttgctctcttcgacgaattattccaagaagaatataccagactttacaga 1472  
Db 541 AGCATGGTGGCCCTTTTACGCAATGCTCTCCAAAGAAAGATGTCAGGACTTTTACAGA 600  
Qy 1473 ggcatacccaactcatgaagtgctccctgcctgtagaactcagttgtagttat 1532  
Db 601 GGCATACCCCAACATTCATGAAAGTGCTCCGCCGTGGCATCAGCTATGAGTGATAT 660  
Qy 1533 gaaatatgaagaactcttagagtagaaccagaatga--tgtagaattttgcttta 1590  
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Qy 1651 agctatgcaaaagaagctgcattttttcacaaaaaggaagcgtlaacaaatggtcac 1710  
Db 773 AGCTATACCAAGAAAGCTG--TTTGCCCTGGCAAGAAAGATGTACCGTGATCAGC 830  
Qy 1711 ttcaaacctttggctaaattatataatgtaacagaagaatggttcaaatcatagtttaagt 1770  
Db 831 TACAAGCCTTTGGGTTACGTTTATACCTTACAGCATGCTGTGAATGCTAGTTCAGATA 890  
Qy 1771 gtttgaagaagccacaactatattactttactttcttaataatacctgcaaatctctgc 1830  
Db 891 GTCAAGAAA--CCACAAAATTTGACTGATTTTTCCTGA-----TAGAGATCTCTCG 940  
Qy 1831 cctgaatccgaaaactgaaatgtactgagcttgaacaaaattggtttgtgtgtagt 1890  
Db 941 CCTGCACCTTAATCTGAAATGTACTGCTGTAGATGAATATTTTGTGTGTAGAT 1000  
Qy 1891 tataatcatlaactcttatttcgggtggttaagttatgcacagttccttatat 1946  
Db 1001 TATAAATCACTAACCTTTGTTGTGATTTGTTCAAGCTCATGTCAATTTTCTTTT 1056  
RESULT 7  
BC019978 2555 bp mRNA linear ROD 22-JAN-2002  
LOCUS BC019978  
DEFINITION Mus musculus, similar to KIAA1896 protein, clone MGC:28954  
ACCESSION BC019978  
VERSION BC019978.1 GI:18043564  
KEYWORDS MGC.  
SOURCE house mouse.  
ORGANISM Mus musculus



LOCUS	BC022114	2576 bp	mRNA	linear	ROD 28-JAN-2002
DEFINITION	Mus musculus, clone MGC:36388 IMAGE:5098924,	complete cds.			
ACCESSION	BC022114				
VERSION	BC022114.1	GI:18380991			
KEYWORDS	MGC.				
SOURCE	house mouse.				
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2576)				
REFERENCE	Strausberg,R. Direct Submission Submitted (24-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgapbs@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@ogsc.bc.ca Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Kirzyski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stolt, Michael Thorne, Miranada Tsai, Natasha van den Bosch, Jill Vardy, George Yang, Scott Zuyerdunyn, Marco Marra.				
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAX Plate: 57 Row: e Column: 23 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Genomescan gene prediction.				
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CDS	BASE COUNT     624 a       675 c       710 g       367 t ORIGIN				
Query Match	20.4%; Score 545.4; DB 10; Length 2576;				
Best Local Similarity	64.9%; Pred. No. 4,7-e-92;				
Matches	807; Conservative 0; Mismatches 436; Indels 0; Gaps 0;				
b1	316 agggagaaatttctactcgagatgcatcaagaatgggaagtgttggaagt 375				
b2					
b3	206 AGCAGAAATTTGTGCAACAGCGTGCACAAGAGCTTGATGGGCACTTGGAAGAGT 265				

QY	376	tttgaagtcttaagaacctatgagaagaataatgttcatttaaggtttaga	435
Db	266	ttgtacatttacctccaagatcatgagaaaaatactggctgtttccaagatctggaca	325
QY	436	aaaaataatgaatgaagaataatgagcttcacgaattgtccagctctccagaacatggtc	495
Db	326	aaaagaatgaatggttcgaattgatgtcttcagagatcatgcagatgcctcgcgagacctgggtg	385
QY	436	tgacattcttgcacaacaacagcagatgttatcttccaaacatgatgttgaatgagaca	555
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QY	556	tgacatgagactggaatgaatggagagactctcttatattaacctgttaacagcatg	615
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QY	616	aggaatattccgtctcttggaacaattctcaacagaaattacaatagaggatgaactta	675
Db	506	cggagatcatctcttacttggaagcacttcacgacttcttcgattgtcgttggaattcgaacg	565
QY	676	ttccagatgaaattcacgcgaaagacgaaanaaaatccgcgaacatgattgagagcagcttgg	735
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Db	806	aaattgcccctgagatccggccatcaaaatttcagcatatgacatgaataacggcttggcgcg	865
QY	976	ctgagaagagcacaanaatggaacatttgagagatttatcttcgttccatagcgttgag	1035
Db	866	gtatgattcaggaacacctgaagatccacgaaaggctttgtgcagagctcttggccggag	925
QY	1036	caactgcacaactctatataatcaatggaggttatgaaacacagcagctggtctgaagca	1095
Db	926	ccatttgcgccacagatgagatctaccacaaatgagagtttgaaagcccgatggccctgcgga	985
QY	1096	aaactgagcagctactctggaatatgatgtggtccagaagaattltgaaacatgaaggct	1155
Db	986	aaacagcgacatgattccggcattctggactgtcccgagagatcttggcattgaaggggtg	1045
QY	1156	tggaagcttttaaaagagctatgtcccaatttatagtaataactatgaatgaagca	1215
Db	1046	tagctgcttcttacaagagcttaatcccaacatgctggggatcatcccttattgctggca	1105
QY	1216	taagatctgctgttatgagctcttcgaatgccattggtctgagatlaattltgcaaaagat	1275
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QY	1276	ctgtlaaacctctgagatcaatgtgtgtcgtggatgctgagcttaccatcagcactgtgtgc	1335
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QY	1336	agctgagcagctaacctatgcttgggttgagaaactgcactgagagctcaagaacatgttag	1395
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QY	1396	aagttctcccaacgtatcatatggttggcctcttcgaagaatttccaaagaagaa	1455
Db	1286	agggcgacactgtagagtaacatagcagcctcttccaacaaagatttgcgcgactgaggggg	1345
QY	1456	taccagagcttataagagatcaaccacaaacttcaagaagtgatccctgtctgaagca	1515

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LOCUS	Sequence 57 from Patent WO0116318.		Linear
DEFINITION	AX092326		
ACCESSION	AX092326.1	GI:13444477	
VERSION			
KEYWORDS			
SOURCE	human.		
ORGANISM	human sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 3334)		
AUTHORS	Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaidi,C.J., Gurney,A.L., Watanabe,C.K. and Wood,W.I.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: WO 0116318-A 57 08-MAR-2001; Genentech, Inc. (US)		
FEATURES	source	1..3334	Location/Qualifiers
BASE COUNT	788 a 848 c 983 g 715 t		
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Best Local Similarity	64.8%;	Pred. No. 9.9e-92;	
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Db	275	TTCGTCATTATCTCCAAAGATCATGAGAAGAGCTGAGCGGTGATTGAATTTTGACA	334
Qy	436	aaaataatgaaataaattgaggtctcagaatgtccaagtctctccagaacatgtgtc	495
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Qy	556	tgaacgtggaactgaaatgaatgagaagactacttctatttaactcctgttaacaagatg	615
Db	455	TGACCATTCAGCTGGAACGAGTGAAGACTTACACCTCTCCACCCCGTGAAGAACATCC	514
Qy	616	aggaattatccgttctcggaaacattctacaaggaatgacatagggaataagctaacta	675
Db	515	CCGAGATCATCTCTACTGGAACATTTCCACGATCTTTGATGTGGGTGAGAAATCTAACGG	574
Qy	676	tccaatgaatcaatcaagaaagcaaaaaaaatccgagacaatgggtggaagcaagcttttg	735
Db	575	TCCCGGATGTGCACAGTGGAGGAAGGACAGCGGGGATGTGTGTGAACACCTGTGTGG	634
Qy	736	caagagcaatgtgtgtgtgtctcgcagacaagacatcccttggagcgtctcgaata	795
Db	635	CAGAGAGTGGGGCAGGGGCCGTATCCAGAACTGCAACGGCCCCCTGGACAGGCTCAAG	694
Qy	796	tcaatgataaggtttcaacggttcaaaatcagacaaaaatgaacatatttggttggtcttcag	855

Db	695	TCCTCATGCAGAGTCCATGCTGCCCTCCGACAGACAACAACATGGGCATCGTGGTGGCTTACATC	754
Qy	856	agatcgttaaagaagagaggtatccgcctcgccttggagagggaatggtatcaaacgltca	915
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Qy	916	aaattcctccctgaagacgctgttaattcttggcctatatagaacagctacaagaagttact	975
Db	815	AAATTGGCCCCCAATCAGGCATCAAAATTCATGGCCCTATGAGCAGATCAAGCCCTGTTGG	874
Qy	976	ctgaagaagacacaaaataaggaacaattggagaagattttctctgttccatcgcgcgtgag	1035
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Qy	1036	caactgcacagacgttttatataataatgaaagttatgaanaaacagcgcgcgtgttagga	1095
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Qy	1096	aaactgggcagttactcttggaatatatgattgtgcgaagaagatttgaacaatgaagct	1155
Db	995	AGACAGGGCCAGTACAGGAATGTCGAGTGGCGCAGGAGATCCCTGGCCAGAGAGGGGG	1054
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Qy	1336	agctggccaagctaccatcgtgcttggtygagaaactcgcataagtcgttaagcactgttag	1395
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RESULT 10			
LOCUS	AB067483	3712 bp	mRNA
DEFINITION	Homo sapiens mRNA for KIAA1896 protein, partial cds.		
ACCESSION	AB067483		
VERSION	AB067483.1	GI:15620850	
KEYWORDS			
SOURCE	Homo sapiens brain cDNA to mRNA, clone:fk06388.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	Nagase,T., Kikuno,R. and Ohara,O.		
TITLE	1 (bases 1 to 3712)		
JOURNAL	Prediction of the coding sequences of unidentified human genes. XXI. The complete sequences of 60 new cDNA clones from brain which code for large proteins		
MEDLINE	DNA research : an international journal for rapid publication of reports on genes and genomes. 8 (4), 179-187 (2001)		
PUBMED	21456161		
REFERENCE	11572484		
AUTHORS	2 (bases 1 to 3712)		
	Ohara,O., Nagase,T. and Kikuno,R.		









sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.  
This clone (DKFZp586G0123) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY. Email: clone@rzpd.de Further information about the clone and the sequencing project is available at <http://www.mips.biochem.mpg.de/proj/cDNA/>.

FEATURES

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BASE COUNT 408 a 174 c 196 g 516 t  
ORIGIN

Query Match 15.1%; Score 403.2; DB 9; Length 1294;  
Best Local Similarity 96.7%; Pred. No. 1.9e-65;  
Matches 433; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

OY 2120 tgggtgaatttcgaaggaagtgatgaataatataatatttcgaatggaactttccat 2179  
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Db 1 TCGTGAATTTCTGAAGGAGAGTGAATATATATTATTTTCAGTGGCAGCTTTCCAT 60  
OY 2180 ttaccacgtaccattatttggctccctggaattatacaactaatttcagtatatactg 2239  
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Db 61 TTTACCACTGTACCAATATTGTTGCTCTGAGTTATACACTAATTTTCAGTATATTACGTG 120  
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Db 121 TTAATTTACCAACACAGGCAATTTATTGAAAGATCCGTTTATCCCTCATTCGCTTTC 180  
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Db 181 AAAACACAGCAGGAAACGAATTCCTGACTGTATCAGCTCTGCAGACATCTTGTGTTT 240  
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Db 301 TGGGACCAATTTCTTAACCTGAATTTCTTTTAATTGCAATGAAGTGGATGATGATC 360  
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Db 361 ACCAATATGATGTGC-TTATTCTCCCTCAGCTGTGAATAT-CTTGAACCTGCTGTTTC 418  
OY 2540 aatatggcagccacaagaaggagaga 2567  
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RESULT 14  
BC005163

LOCUS BC005163 2757 bp mRNA linear PRI 12-JUL-2001  
DEFINITION Homo sapiens, clone IMAGE:3530123, mRNA, partial cds.  
ACCESSION BC005163  
VERSION BC005163.1 GI:13477372  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 2757)  
AUTHORS Strausberg, R.  
JOURNAL Direct Submission  
Submitted (26-MAR-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

REMARK

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbioology.org>  
contact: [amadansystemsbiology.org](mailto:amadansystemsbiology.org)  
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia  
Greene, Mark Kettelman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
Series: IRAL Plate: 11 Row: e Column: 21  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Hexamer frequency ORF  
analysis.

FEATURES

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BASE COUNT 599 a 710 c 843 g 605 t  
ORIGIN

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Matches 581; Conservative 0; Mismatches 326; Indels 0; Gaps 0;

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Db 79 GGATGTGTTGGAGACACCTGTTGGCAGAGGTGGCAGGCGCCATTCACAGAACCTGGA 138  
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Db 139 CGGCCCCCTGGACAGGCTCAAGGTGCTCATGAGTCCATGCTCCCGACACACACAA 198



Oy	832	tgaacatcttggctggtccttcagcaagatgfytaaaagaaggagatgcgcctcgcttgga	891
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Db	559	TGGGCATCATCCCTATGCTCGGCATCGACTTGTGAGTCTAGAGACGCTCAAGATGGCT	618
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DEFINITION	Sequence 471 from Patent WO0196388.		
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ORGANISM	human.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	Jiang,Y., Harlocker,S.L. and Secrist,H. Compositions and methods for the therapy and diagnosis of colon cancer		
JOURNAL	Patent: WO 0196388-A 471 20-DEC-2001.		
FEATURES	CORIXA CORPORATION (US)		
source	Location/Qualifiers		
	1..578		

	BASE COUNT	167 a	98 c	88 g	222 t	3 others
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Query Match	12.4%;					
Best Local Similarity	96.0%;					
Matches 362; Conservative	0;					
Mismatches 13; Indels 2; Gaps 2						
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Qy 2251	acacaaagcaatttalttgaagatccglttatccctgcattgcttgaagaagcag	2310				
Dd 61	ACACAAGCAATTATTTGAAGATTCGCTTATCCTGCATTCGTTGAAAAGCAGCAG	120				
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Dd 121	GAAAGCAATTCCTTGACCTGTATCAGCTTCGCAGAGCATCTTTGTTCCCTTGTCTCT	180				
Qy 2371	tgcttcctcaacttttgaatcagatccglttttagcagaagaactcttggagaccatc	2430				
Dd 181	TGTGTTCCATCTTTGGAATTCAGATTCGCTTTTAGTCAGAAAGACTTCTTGGACCATTC	240				
Qy 2431	ttagtaacctgaattctctttaaaltcatgaagtgatgatcatagacaagtgcac	2490				
Dd 241	TTAGTAACCTGAAATTTCTTTTAAATTCATGAAGATGGATGATCATGAGCAAAATGATG	300				
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Dd 359	CACAAAGGTGAGAGATA 375					

Search completed: August 18, 2002, 08:23:49  
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Matches 362; Conservative 0; Mismatches 13; Indels 2; Gaps 2.

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QY 2251 aacaaaggaattatttgaagaattccggttatccctgcacattgcttttgaagaagcagcg 2310
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QY 2311 gaaacgaatttttgaacttgatcacagctctcgcagaagacatcttgttcccttgctc 2370
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QY 2371 ttggttcctacctttgaaacgattccglttttagtcaggaagactccttgggaccatc 2430
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QY 2431 ttagtaacctggaattctctttttaaattgcatggaagtgtatgatcatgacgaagtgtatg 2490
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Db 241 TTAGTAACTCGAAATTTCTTTTAAATTGCATGAAAGTGGATGATCATAGCAAAATGATG 300
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QY 2491 ggccttattctccctcactggtgaaatccttgaacttgctglttgcaatatgggcag 2550
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Db 301 TGC-TTATTTCTCCCTCACTGTGAAATAT-CATTGAACTTGCTGTTTCAATATGGGCGAG 358
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Search completed: August 18, 2002, 08:23:49
Job time: 19296 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 18, 2002, 06:27:16 ; Search time 293.03 Seconds  
(without alignments)  
15661.578 Million cell updates/sec

Title: US-09-777-921A-1  
Perfect score: 2673  
Sequence: 1 ccgcacaccggcagcgccccc.....atacaatcatgatctctg 2673

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2428	90.8	384	22	AAK52210 Human polynucleoti
2	943.6	35.3	1090	21	AAC77660 Human cancer assoc
3	730.8	27.3	757	22	AA163830 Human polynucleoti
4	549.4	20.6	3237	22	AA531626 CDNA encoding nove
5	545.4	20.4	1808	22	AA159228 Human polynucleoti
6	545.4	20.4	1816	21	AA61789 Skin cell CDNA, SE
7	545.4	20.4	1816	22	AA61789 Skin cell CDNA, SE
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9	543.8	20.3	3333	21	AA65058 Membrane-bound pro

10	543.8	20.3	3334	22	AA692086 Human PRO1106 CDNA
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12	540.2	20.2	549	22	AAK53194 Human polynucleoti
13	534.2	20.0	2625	22	AA544597 Human full-length
14	534.2	20.0	2644	22	AA544769 Human contig polyn
15	494.4	18.5	1481	21	AAC76538 Human ORFX ORE2093
16	470	17.6	1616	23	AA586824 DNA encoding novel
17	436	16.3	1386	22	AA166981 Human membrane tra
18	436	16.3	1929	22	AA166980 Human membrane tra
19	355	13.3	1246	21	AAC90462 Human uncoupling p
20	337.2	12.6	997	21	AA61628 Skin cell CDNA, SE
21	337.2	12.6	997	22	AAC99561 Human full-length
22	277.8	10.4	2282	22	AAK94158 Human polynucleoti
23	276.4	10.3	2502	22	AA161014 Human CDNA 5'-end
24	269.4	10.1	713	22	AAK91636 Human CDNA clone I
25	269.4	10.1	713	22	AAK93552 Human uncoupling p
26	246.8	9.2	2517	21	AAC90463 Human uncompling p
27	184	6.9	2340	22	AA61876 Human foetal liver
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29	173.6	6.5	576	22	AAK36087 Human bone marrow
30	173.6	6.5	576	22	AAK36087 Human bone marrow
31	173.6	6.5	576	22	AA11802 Novel human diagno
32	171.6	6.4	396	22	AA539187 DNA encoding novel
33	170.6	6.4	417	23	AA586821 Novel human diagno
34	168.8	6.3	400	22	AA539183 Human foetal liver
35	168	6.3	168	22	ABA74371 Human brain expres
36	168	6.3	168	22	AAK2838 Human bone marrow
37	168	6.3	168	22	AAK9009 Human bone marrow
38	168	6.3	168	22	AA154837 Probe #23523 used
39	163.2	6.1	717	21	AAC76528 Human ORFX ORE2083
40	161	6.0	506	22	ABA61739 Human foetal liver
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## ALIGNMENTS

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XX 06-NOV-2001 (first entry)	
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DE	
XX	
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;	
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;	
KW tissue growth factor; immunomodulatory; cancer; leukaemia;	
KW nervous system disorder; arthritis; inflammation; ss.	
XX	
OS Homo sapiens.	
XX	
PN WO200157190-A2.	
XX	
PD 09-AUG-2001.	
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PF 05-FEB-2001; 2001WO-US04098.	
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PR 03-FEB-2000; 2000US-0496914.	
PR 27-APR-2000; 2000US-0560875.	
PR 20-JUN-2000; 2000US-0598075.	
PR 19-JUL-2000; 2000US-0620325.	
PR 01-SEP-2000; 2000US-0654936.	
PR 15-SEP-2000; 2000US-0663561.	
PR 20-OCT-2000; 2000US-0693325.	
PR 30-NOV-2000; 2000US-0728422.	
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PA (HXSE-) HXSEQ INC.  
XX  
XX Tang YT, Liu C, Dmanac RT, Asundi V, Zhou P, Xu C, Gao Y, Ma Y;  
PI Zhao OA, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Wehrman T, Goodrich R;  
XX WPI: 2001-476283/51.  
DR P-PSDB; AAM79077.  
XX  
PT Nucleic acids encoding polypeptides with cytokine-like activities,  
useful in diagnosis and gene therapy -  
XX  
XX Claim 1; Page 2526-2529; 6221pp; English.  
PS  
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
CC encoded polypeptides (AAM78333-AAK80302) that exhibit activity elating to  
CC cytokine cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation.  
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
CC (AAM800020) are omitted as the relevant pages from the sequence listing  
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XX  
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SQ

Query Match 90.8%; Score 2428; DB 22; Length 3384;  
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Db 1843 aaattgtttgtgtgtgagttataaatcatattcttacttcgggtgttactgct 1902  
QY 1928 tatggcaagttccttatattttaaattctgttttatatatattggaatgcttataag 1987  
Db 1903 tatggcaagttccttatattttaaattctgttttatatatattggaatgcttataag 1962  
QY 1988 ttctttaaatttccatataagaaacatataagaataatcatattataataataccta 2047  
Db 1963 ttctttaaatttccatataagaaacatataagaataatcatattataataataccta 2022  
QY 2048 cagcaaaagcatccaaataagataggtttatgtccctaatttccccaagctgaatc 2107  
Db 2023 cagcaaaagcatccaaataagataggtttatgtccctaatttccccaagctgaatc 2082  
QY 2108 gaatgaacagatggtggaatttctgaagggaagtatgaataattatatttctgaag 2167  
Db 2083 gaatgaacagatggtggaatttctgaagggaagtatgaataattatatttctgaag 2142  
QY 2168 gcaatttccatatttcaacctgtacacattatgtgtccctgagttatacaactaatttc 2227  
Db 2143 gcaatttccatatttcaacctgtacacattatgtgtccctgagttatacaactaatttc 2202  
QY 2228 agtatatactgttaataatcaccaacaaaggcaattatattgaaagatccgcttact 2287  
Db 2203 agtatatactgttaataatcaccaacaaaggcaattatattgaaagatccgcttact 2262  
QY 2288 gccattgctttgaaagcagcaggaagaatttttgaactgtatccagcttcgcaga 2347  
Db 2263 gccattgctttgaaagcagcaggaagaatttttgaactgtatccagcttcgcaga 2322  
QY 2348 gcaatttcttcttctgttccctgttttcttacttcttgaatcagatccgcttactg 2407  
Db 2323 gcaatttcttcttctgttccctgttttcttacttcttgaatcagatccgcttactg 2382  
QY 2408 aggaagactcttggagcaattcttagtaacctgaaattctttttaaattgacgaagt 2467  
Db 2383 aggaagactcttggagcaattcttagtaacctgaaattctttttaaattgacgaagt 2442  
QY 2468 ggaatgatcatagcaagatgagtggtttatttctccccaactggtgaatattcttga 2527  
Db 2443 ggaatgatcatagcaagatgagtggtttatttctccccaactggtgaatattcttga 2500  
QY 2528 ctgtcgtttgcaatattggcagccacaaaggggagaga 2567  
Db 2501 ctgtcgtttgcaatattggcagccacaaaggggagaga 2540

RESULT 2  
AAC77660  
ID AAC77660 standard; cDNA, 1090 BP.  
XX  
AC AAC77660;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human cancer associated gene sequence SEQ ID NO:54.  
XX  
KW Human: cancer associated gene; cancer antigen; detection; cancer;  
diagnosis; cytostatic; proliferative; vulnerability; immunomodulator;  
antidiabetic; antiallergic; antineoplastic; antitumor; antiviral;  
antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;

KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;  
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;  
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
KW allergic reaction; graft versus host disease; organ rejection;  
KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
KW neurological disease; drug screening; ss.  
XX  
OS Homo sapiens.  
PN MO200055350-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 08-MAR-2000; 2000MO-US05882.  
XX  
PR 12-MAR-1999; 99US-0124270.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PI Rosen CA, Ruben SM;  
XX  
DR MPI, 2000-587533/55.  
XX  
DR P-PSDB; AAB43451.  
XX  
PT Novel isolated nucleic acids comprising sequences encoding peptides  
XX useful for treating or diagnosing e.g. cancer -  
XX  
PS Claim 1; Page 651; 2352pp; English.  
XX  
XX AAC77607 to AAC78448 encode the human cancer associated proteins given  
CC in AAB4398 to AAB44239. The proteins can have activities based on the  
CC tissues and cells the genes are expressed in. Example of activities  
CC include: cytostatic; proliferative; vulnerability; immunomodulator;  
CC antidiabetic; antiallergic; antineoplastic; antitumor;  
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;  
CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The  
CC polynucleotides and polypeptides can be used for preventing, treating or  
CC ameliorating medical conditions and diagnosing pathological conditions.  
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
CC the present invention may be used to treat immune disorders by activating  
CC or inhibiting the proliferation, differentiation or mobilisation of  
CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
CC disorders, allergic reactions, graft versus host disease and organ  
CC rejection, modulate haemostatic or thrombolytic activity, modulate  
CC inflammation, cancers, cardiovascular disorders, neurological disease and  
CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
CC the present invention.  
XX  
SQ Sequence 1090 BP; 328 A; 175 C; 174 G; 411 T; 2 other;

Query Match 35.3%; Score 943.6; DB 21; Length 1090;  
Best Local Similarity 98.2%; Pred. No. 3.9e-202;  
Matches 996; Conservative 0; Mismatches 14; Indels 4; Gaps 4;

QY 1555 gagtaaccagaatgatgttgaatttttggcttagctcgatgaatgtgaacttcaaca 1614  
Db 1 1 gagtaaccagaatgatgttgaatttttggcttca-ctgatatattgaaactttcaca 59  
QY 1615 atctcggagtgacttttctcctcgatggaacaagctatagcgaagaagctgcat 1674  
Db 60 atctcggagtgacttttctcctcgatggaacaagctatagcgaagaagctgcat 119  
QY 1675 tttttccaaaagggaagacggtaacaatgctcaacttttggcctaattata 1734  
Db 120 tttttccaaaagggaagtgtaacaatgctcaacttttggcctaattata 179  
QY 1735 tgaacacagaatgctcaaatcatagtttaattgttttgaagaagccacaaattat 1794  
Db 180 tgaacacagaatgctcaaatcatagtttaattgttttgaagaagccacaaattat 239

OY 1795 acttatactttcttaataatccctcgaacatctcgcctt-gaatccgaatctgaaatg 1853  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 240 acttatactttcttaataatccctcgaacatctcgccttcccggaatccgaatctgaaatg 299  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 1854 tactggtctgaaacaaattgttctgtgtataggtataatcaatcaatcttatttc 1913  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 300 tactggtctgaaacaaattgttctgtgtataggtataatcaatcaatcttatttc 359  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 1914 ggggtgttaagttatgacaggttcccttataatttaattcttctgtttatatttga 1973  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 360 ggggtgttaagttatgacaggttcccttataatttaattcttctgtttatatttga 419  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 1974 atgctctatagattcttcttaattcttcccttataagaaacattatagaaacattatcga 2033  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 420 atgctctatagattcttcttaattcttcccttataagaaacattatagaaacattatcga 479  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 2034 taaataatacttaccagcaaaagcatccaataagttataggtttatgtcctattttc 2093  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 480 taaataatacttaccagcaaaagcatccaataagttataggtttatgtcctattttc 539  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 2094 ttccagctgtaacgaatgaacacagtggtgaattctgaaggaggtatgaattat 2153  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 540 ttccagctgtaacgaatgaacacagtggtgaattctgaaggaggtatgaattat 599  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 2154 atttactcaagtgagcactttccatttaccacgttacocatatttggctcctgaagt 2213  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 600 atttactcaagtgagcactttccatttaccacgttacocatatttggctcctgaagt 659  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 2214 ataacataatttcagttatattactgtttaattaccacacacaggaatttttgaag 2273  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 660 ataacataatttcagttatattactgtttaattaccacacacaggaatttttgaag 719  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 2274 attcggttatattccgcattctgttgaagaagcagcaggaagaatttttgaattga 2333  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 720 attcggttatattccgcattctgttgaagaagcagcaggaagaatttttgaattga 779  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 2334 tcagctctcagagacacattgttcttcttcttcttcttcttcttcttcttcttcttct 2393  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 780 tcagctctcagagacacattgttcttcttcttcttcttcttcttcttcttcttcttct 839  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 2394 attcggttatattccgcattctgttgaagaagcagcaggaagaatttttgaattga 2433  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 840 attcggttatattccgcattctgttgaagaagcagcaggaagaatttttgaattga 899  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 2454 taattgcataagtgatgatactgagcaagtgatggcttatttctcctcaactggt 2513  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 900 taattgcataagtgatgatactgagcaagtgatggcttatttctcctcaactggt 2513  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 OY 2514 gaataatccttgaactgctgttgcataatggcagcccaaaaggaggagaga 2567  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 959 gaataatccttgaactgctgttgcataatggcagcccaaaaggaggagaga 1011  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 3  
 AAI63830  
 ID AAI63830 standard; cDNA: 757 BP.

AC AAI63830;

DT 22-OCT-2001 (first entry)

DE Human polynucleotide SEQ ID NO 38.

KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;  
 KW cerebroprotective; nootropic; neuroprotective; immunosuppressive; antiviral;  
 KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;  
 KW neuroprotective; antiallergic; hepatotropic; antidiabetic;  
 KW antiinflammatory; antitumor; anticonvulsant; antibacterial;  
 KW antiparasitic; cardiac; gene therapy; cancer; immune disorder;  
 KW cardiovascular disorder; neurological disease; infection; human; ss.  
 OS Homo sapiens.

XX  
 PN W0200155308-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 17-JAN-2001; 2001WO-US01309.  
 XX  
 PR 31-JAN-2000; 2000US-0179065.  
 PR 04-FEB-2000; 2000US-0180628.  
 PR 24-FEB-2000; 2000US-0184664.  
 PR 02-MAR-2000; 2000US-0186350.  
 PR 16-MAR-2000; 2000US-0189874.  
 PR 17-MAR-2000; 2000US-0190076.  
 PR 18-MAR-2000; 2000US-0198123.  
 PR 19-MAY-2000; 2000US-0205515.  
 PR 07-JUN-2000; 2000US-0209467.  
 PR 28-JUN-2000; 2000US-0214886.  
 PR 30-JUN-2000; 2000US-0215135.  
 PR 07-JUL-2000; 2000US-0216647.  
 PR 07-JUL-2000; 2000US-0216880.  
 PR 11-JUL-2000; 2000US-0217487.  
 PR 14-JUL-2000; 2000US-0217496.  
 PR 26-JUL-2000; 2000US-0218290.  
 PR 26-JUL-2000; 2000US-0220963.  
 PR 14-AUG-2000; 2000US-0220964.  
 PR 14-AUG-2000; 2000US-0224518.  
 PR 14-AUG-2000; 2000US-0224519.  
 PR 14-AUG-2000; 2000US-0225213.  
 PR 14-AUG-2000; 2000US-0225214.  
 PR 14-AUG-2000; 2000US-0225266.  
 PR 14-AUG-2000; 2000US-0225267.  
 PR 14-AUG-2000; 2000US-0225268.  
 PR 14-AUG-2000; 2000US-0225270.  
 PR 14-AUG-2000; 2000US-0225447.  
 PR 14-AUG-2000; 2000US-0225757.  
 PR 14-AUG-2000; 2000US-0225758.  
 PR 18-AUG-2000; 2000US-0225759.  
 PR 22-AUG-2000; 2000US-0226279.  
 PR 22-AUG-2000; 2000US-0226681.  
 PR 22-AUG-2000; 2000US-0226868.  
 PR 23-AUG-2000; 2000US-0227182.  
 PR 30-AUG-2000; 2000US-0227809.  
 PR 01-SEP-2000; 2000US-0228924.  
 PR 01-SEP-2000; 2000US-0229287.  
 PR 01-SEP-2000; 2000US-0229343.  
 PR 01-SEP-2000; 2000US-0229344.  
 PR 01-SEP-2000; 2000US-0229345.  
 PR 05-SEP-2000; 2000US-0229509.  
 PR 05-SEP-2000; 2000US-0229513.  
 PR 06-SEP-2000; 2000US-0230437.  
 PR 06-SEP-2000; 2000US-0230438.  
 PR 08-SEP-2000; 2000US-0231242.  
 PR 08-SEP-2000; 2000US-0231243.  
 PR 08-SEP-2000; 2000US-0231244.  
 PR 08-SEP-2000; 2000US-0231413.  
 PR 08-SEP-2000; 2000US-0231414.  
 PR 08-SEP-2000; 2000US-0232080.  
 PR 12-SEP-2000; 2000US-0232081.  
 PR 12-SEP-2000; 2000US-0231968.  
 PR 14-SEP-2000; 2000US-0232397.  
 PR 14-SEP-2000; 2000US-0232398.  
 PR 14-SEP-2000; 2000US-0233399.  
 PR 14-SEP-2000; 2000US-0233400.  
 PR 14-SEP-2000; 2000US-0232401.  
 PR 14-SEP-2000; 2000US-0233063.  
 PR 14-SEP-2000; 2000US-0233064.  
 PR 14-SEP-2000; 2000US-0233065.  
 PR 21-SEP-2000; 2000US-0234223.  
 PR 21-SEP-2000; 2000US-0234274.  
 PR 25-SEP-2000; 2000US-0234997.  
 PR 25-SEP-2000; 2000US-0234998.  
 PR 26-SEP-2000; 2000US-0235484.  
 PR 27-SEP-2000; 2000US-0235854.

[illegible]

PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI, 2001-488781/53.  
DR P-PSDB; AAM43524.  
XX  
PT New isolated nucleic acids and polypeptides, useful for diagnosing,  
PT treating and/or preventing human diseases and disorders -  
XX  
PS  
PS Claim 1; SEQ ID NO 38; 664bp + Sequence Listing; English.  
XX  
CC The invention relates to human polynucleotides (AA163803-AA164012) and  
CC the encoded proteins (AAM434497-AA43660) useful for preventing, treating  
CC or ameliorating medical conditions e.g. by protein or gene therapy. The  
CC genes were isolated from a range of human tissues disclosed in the  
CC specification. The nucleic acids, proteins, antibodies and (anti)agonists  
CC are useful in the diagnosis, treatment and prevention of: (a) cancer  
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,  
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or  
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,  
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,  
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
CC colitis; (c) cardiovascular diseases such as myocardial ischaemias;  
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
CC and parasitic infections.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at [ftp.wipo.int/pub/published\\_pat\\_sequences](http://ftp.wipo.int/pub/published_pat_sequences).  
XX  
XX Sequence 757 BP; 214 A; 154 C; 209 G; 173 T; 7 other;

	Query Match	27.3%	Score 730.8;	DB 22;	Length 757;	
	Best Local Similarity	98.4%;	Pred. No. 2.1e-154;			
	Matches 743;	Conservative 3;	Mismatches 8;	Indels 1;	Gaps 1;	
OY	100 gtagcttcttcgagccaggccgcgtcctcgctcgggaaccatgttgccgtgcgtcgagact	159				
Dd	2 gtgacctcttcgcccaggccgctcgtgcctctcggaacattgtttgcgtgcgtcgagact	61				
OY	160 tgcgcgtgcccaacgcgcgcgtcgtccagaagcacgcagccgcgtacagaccctct	219				
Dd	62 tcgtgtctgcccaacgcgcgncctgcagagacgcgagcagccgacgcgtacagaccctct	121				
OY	220 tccaggaactcygaccgcaatgggagcggagtgtgtgacatcgcgcgactgcagaggggc	279				
Dd	122 tccaggcactcgtgaccgcgcgaatgggagcggagtgtgtgacatcgcgcgactgcagaggggc	181				
OY	280 tcaaggaaccttggaactccctctcgccgcagagcccgaggaagaaattttactactgag	339				
Dd	182 tcaaggaaccttggaactccctctggccgcagagcccgaggaagaaattttactactgag	241				
OY	340 atgtcaacaagaatlyggaagctggaattttggaaatlttatgaagtaacctlaagaacatg	399				
Dd	242 atgtcaacaagaatlyggaagctggaattttggaaatlttatgaagtaacctlaagaacatg	301				
OY	400 agaagaataatyaatatlygcatltaaagatttaagacaaaataatyaatygaanaaatlgag	459				
Dd	302 agaaagaataatyaatatlygcatltaaagattttagacaaaaataatyaatygaanaaatlgag	361				
OY	460 ctccgaagaattgtccagcgtctccagaaacacgggtcgtactatttctgaacaacaagcag	519				
Dd	362 ctccgaagaattgtccagcgtctccagaaacacgggtcgtactatttctgaacaacaagcag	421				
OY	520 agtgtatcttccaagaacatlygatgttgaatgggacaatgacagtygacatygaaatlyga	579				
Dd	422 agtgtatcttccaagaacatlygatgttgaatgggacaatgacagkygacatygaaatlyga	481				
OY	580 gagactactcttatttaaacctcgtttaagaacatlygagaatratatccgtttctygaac	639				
Dd	482 gagactactcttatttaaacctcgtttaagaacatlygagaatratatccgtttctygaac	541				
OY	640 atttcaacggaaatlacaaatagqqaatagcttaactatccagatbaaattcaacqqaaacq	699				

|||||  
Db 542 attctacagggaattgcaactaaggaggatgcttaactatcccgatgaaltccaggaagacg 601  
QY 700 aaaaaaacccgacaatggtgagggacgctttggcagggagcatctgtctgtct 759  
Db 602 aaaaaaacccgacaatggtgagggacgctttggcagggagcatctgtctgtctgct 661  
QY 760 ctgcgaacaagcactgccccttggacgctctgaaatcatgatgcaggttcaaa 819  
Db 662 ctngacaagcactgccccttggacgctctgaaatcatgatgcaggtt-acgggtcaa 720  
QY 820 aatcagacaataatgaatattgttgcttgcga 854  
Db 721 aatcagacaataatgaatattgttgcttgcga 755  
RESULT 4  
AAS31626  
ID AAS31626 standard; cDNA; 757 BP.  
XX AAS31626;  
AC AAS31626;  
DT 04-DEC-2001 (first entry)  
XX  
DE cDNA encoding novel human calcium-binding protein #50.  
XX  
XX Human; calcium-binding protein; calcium flux; neurological disease;  
KW immune dysfunction; digestive disorder; neoplastic disease;  
KW blood disorder; infectious disease; gene therapy; immunosuppressive;  
KW antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;  
KW virucide; ss.  
XX  
OS Homo sapiens.  
XX  
PN W0200155304-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01302.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
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PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
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PR 22-AUG-2000; 2000US-0227182.  
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PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
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PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
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PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
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PI Rosen CA, Barash SC, Ruben SM;  
XX  
DR WPI; 2001-465568/50.  
DR P-PSDB; AAU19941.

PT Isolated nucleic acid molecule encoding a calcium-binding protein is  
PT used in preventing, treating or ameliorating a medical condition -  
XX  
Claim 4; SEQ ID No 60; 542pp; English.  
PS

CC The present invention relates to the isolation of novel human  
 CC calcium-binding proteins (AA019692-AA019693), and cDNA and genomic  
 CC sequences encoding for these proteins. The sequences of the invention  
 CC are useful in the diagnosis, prevention and/or prognosis of diseases  
 CC associated with aberrant calcium flux. Such disorders include  
 CC neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),  
 CC immune dysfunction (e.g. severe combined immunodeficiency, SCID),  
 CC digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic  
 CC disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or  
 CC infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The  
 CC novel calcium-binding proteins are also useful as screening tools to  
 CC identify antagonists and/or agonists that may enhance or inhibit  
 CC activities mediated by calcium-binding proteins. The polynucleotides of  
 CC the invention are also useful in gene therapy. AAS31577-AAS31654  
 CC represent cDNA sequences encoding for the novel human calcium-binding  
 CC proteins.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).  
 CC  
 CC Sequence 757 BP; 214 A; 154 C; 209 G; 173 T; 7 other:

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OY	220	tccaagcaccttgacccgaatttgggaacggagatgtgtggacacatcggcggagcttgcagagagggc	279
Db	122	tccaagcaccttgacccgaatggggagacggagatgtgtggacacatcggcggagcttgcagagagggc	181
OY	280	tcaaggaaacctggagcatccctctcggccacaggaagcgcggagggagaaaacttttaactacggag	339
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OY	580	gagactacttcttctaaccctttagacagacattggagaattatccgctttcttggaaac	639
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OY	700	aaaaaaaaatccggagcaatgvtgvggggagcgttttggagaagagacattgctgtgtgcgtct	759
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KW	Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer		
KW	peripheral nervous system; neuropathy; central nervous system; CNS;		
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;		
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;		
KW	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;		
KX	leukemia; ss.		
OS	Homo sapiens.		
PN	WO200153312-A1.		
XX	26-JUL-2001.		

RESULT	5
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KW	peripheral nervous system; neuropathy; central nervous system; CNS;
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KW	chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW	leukaemia; ss.
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OS	Homo sapiens.
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PN	WO20015312-A1.
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PD	26-JUL-2001.
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DE	cDNA encoding murine ADP/ATP transporter family protein, SEQ ID NO:262		
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KW	embryonic skin cell; keratinocyte stem cell; transcrit amplifying cell;		
KW	secreted; transmembrane; inflammation; cancer; neurological disease;		





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XX      XX      (GETH ) GENETECH INC.
XX      PA
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PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J;  
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DR P-PSDB; AAY66718.  
XX  
PT Membrane-bound proteins and related nucleotide sequences -  
XX  
PS Claim 2; Fig 205; 822pp; English.  
XX  
CC The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIR  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
CC will also be useful for the preparation of PRO polypeptides, especially  
CC by recombinant techniques.  
XX  
SQ Sequence 3333 BP; 787 A; 848 C; 983 G; 715 T; 0 other;

Query Match 20.3%; Score 543.8; DB 21; Length 3333;  
Best Local Similarity 64.8%; Pred. No. 4.1e-112;  
Matches 806; Conservative 0; Mismatches 437; Indels 0; Gaps 0;

QY 316 agagaagaatttactactgagatgcatacaagaatggaagcgtgatttgaagaat 375  
DB 215 agagaagaatttgcacaagctggagataaagacctgtgaggcagacttgaagaat 274  
QY 376 ttatgaagtaaccttaagaaccatgatagaagaataatgagcatltaagatttgaaca 435  
DB 275 ttgtcattatattcccaagatcatgatagaagcttgagcgtgttattgaattttgaca 334  
QY 436 aaaaataatgagaaaattgagcttcagaatgtccagctctccacagacatgtgtc 495  
DB 335 aaaaagatgatgacgatgcacgcagagagatcaltgcctccgtcggacttggag 394  
QY 496 tgactattctgaacaacagcagatgattcttcaaaagcatgtgttattgagacaa 555  
DB 395 tcaagatattcgaacagcagcagcaaaaattctcaagcattgataaaaacgcagca 454  
QY 556 tgacaatgagcttgaatgaatgagagactacttctatttaaccgtttacagacatg 615  
DB 455 tgaccatgcagctggaacgagtgagagactataccaactcctccacccttggaaaaatcc 514  
QY 616 aggaattatccgttctctggaacattctacaggaattacatagaggatgacttaacta 675  
DB 515 ccgagatcatctctacttgaagcattccacgacttcttgatgtgggtgaagaatctaa 574  
QY 676 ttccagaataattcacgaggaagcaaaaaaacccggaacaattgtgaggcagcttttg 735  
DB 575 tcccgatgatgttcaacagtggagagagagagagagagatgtgtgagacaccctgtg 634  
QY 736 caggaagcatlgtcgtgtgtctgtctcgaacaagcactccctcttgagaccgtctaa 795  
DB 635 caggaagtgtgggagggcgctgtatccagaacctgcgcccccccgagacagctcaag 694  
QY 796 tcatgtatgaggttcacggtttcaaatcagcaaaaatgaacataattgtgtcttcgac 855  
DB 695 tgcctcatgaagtccatgtctcccgacagacaacatgagcatcgttgtgtgttcaact 754  
QY 856 agatgttaaaagagaggtatccgtcttggaggggaaattgataaaagttacata 915  
DB 755 agatgttctgagaagaagagggccaggtcaactctgtgcggggcaattgcatlcaacg 814  
QY 916 aaattgtctctgagacagctgttaattctgtggcatatgatacagagatttactta 975

DB 815 aaattgtccccgaatcagcgcacatcaaatctatgagcttatgagcagataaagcgtctgt 874  
QY 976 ctgaagaagacaataaattggaacatttgaagattattctgtgtccatgtgtgag 1035  
DB 875 gtagtgaccagagactctgtagatattcagagagcttgtgtgacaggttcccttgca 934  
QY 1036 caactgacagactttatattccaaatgagatgagatgaagaacagcgtgtgtgagca 1095  
DB 935 ccatacgccagagcagcatcaccacaaatgaggtcccgaaagaccggtatgtgcctgagca 994  
QY 1096 aaactggcagactcctcgaatatatattgtgcgaagaagattttaaataaagct 1155  
DB 995 agacagggcagactactcagatgtgtgactgcgcgcaagagatctctgtccagaaaggg 1054  
QY 1156 tggagacttttacaagaagctatgttcccaattattatagatatacatcctatgagca 1215  
DB 1055 tggcgcctctacaagaagctatgttcccaaatgcatgcgggcatcatccctatgcgca 1114  
QY 1216 tagatctgtgtgtatgagctcttgaagtcctatgtcgtgagataatttgaagaagat 1275  
DB 1115 tcgaaccttgacgtcagagagcgtcaagaatgtcctgtgcagactatgtcagtgaca 1174  
QY 1276 ctgtaaaccttgagatcatgtgtgtgtgagatgcgtgtccttaaccagaccgtgtgtc 1335  
DB 1175 gcgcgagaccggcggtgtgtgtgtctcctgtcctgtgtgacacatgtccagatccgtgtcc 1234  
QY 1336 agcttggcagactcaccatgtgcttggtagaactgcagtgcaggtcaagcattgag 1395  
DB 1235 agcttggcagactcaccctgtgccttgcagacccggtatgcagggcgcaagcctctatg 1294  
QY 1396 aaggttccccaagcgtggaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1455  
DB 1295 agggcgtccggaggtgacatgagcagcctctcaacatattccttgcgagccgagggg 1354  
QY 1456 taccagagacttaccagagcatcaccacaaactcattgaatgagtgctccctgttgaagca 1515  
DB 1355 ccttgcggtcgtacagggggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1414  
QY 1516 tcaattatgtgttattgaataatataatgaagcaaataggagt 1558  
DB 1415 tcagctacgtgtgtacagaaacttgaagatcaaccttgccttggcgt 1457

RESULT 10  
AAF92086 standard; cDNA; 3334 BP.  
XX  
AC AAF92086;  
XX  
DT 15-MAY-2001 (first entry)  
XX  
DE Human PRO1106 cDNA.  
XX  
KW Human; PRO protein; mapping; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200116318-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 24-AUG-2000; 2000MO-US23328.  
XX  
PR 01-SEP-1999; 99MO-US20111.  
PR 15-SEP-1999; 99MO-US21090.  
PR 07-DEC-1999; 99US-0169490.  
PR 09-DEC-1999; 99US-0170262.  
PR 11-JAN-2000; 2000US-0175481.  
PR 18-FEB-2000; 2000MO-US04341.  
PR 18-FEB-2000; 2000MO-US04342.  
PR 22-FEB-2000; 2000MO-US04414.  
PR 01-MAR-2000; 2000MO-US05601.



PR 03-MAR-2000; 2000US-0187202.  
PR 25-APR-2000; 2000US-0199397.  
PR 22-MAY-2000; 2000MO-US14042.  
PR 05-JUN-2000; 2000US-0209832.  
XX  
XX (GERTH ) GEMENTECH INC.  
XX  
XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WJ;  
XX  
XX WPI; 2001-183260/18.  
DR P-PSDB; AAB87554.  
XX  
XX Eighty four nucleic acids encoding PRO polypeptides, useful in  
PT molecular biology, including use as hybridization probes, and in  
PT chromosome and gene mapping.  
XX  
XX  
PS Claim 2; Fig 57; 278pp; English.  
XX  
XX The present sequence is the coding sequence for a human PRO polypeptide  
CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO  
CC antagonists or anti-PRO antibodies are useful for preparation of a  
CC medicament useful in the treatment of a condition which is responsive to  
CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO  
CC protein may also be employed as molecular weight markers for protein  
CC electrophoresis. The PRO coding sequence has applications in molecular  
CC biology, including use as hybridisation probes, and in chromosome and  
CC gene mapping.  
XX  
SQ Sequence 3334 BP; 788 A; 848 C; 983 G; 715 T; 0 other;

Query Match 20.3%; Score 543.8; DB 22; Length 3334;  
Best Local Similarity 64.8%; Pred. No. 4.1e-112;  
Matches 806; Conservative 0; Mismatches 437; Indels 0; Gaps 0;  
QY 316 agagagaatttttactactgagatgtaacaagaatggaagctgatttgaagaat 375  
DB 215 agcagaataatttacaagctggaagaaagacctgtatgagcagctagaacttgaagaat 274  
QY 376 ctatgaagtaaccttaagaagccatgagaagaataatggaatgacatlaagattgaga 435  
DB 275 tgttcattatctccaaagatcatgagaagaagctgagctgtgtttaaagatttggaca 334  
QY 436 aaaaataatgagaaaatgaggttcagaatctgcagctctccagacactggtc 495  
DB 335 aaaaagatgatgacgactgagcgcagagatcatgacgccctgcggaacttggag 394  
QY 496 tgactattctgaacaacagagattgattcttcaagaagcattgtgttgaagaca 555  
DB 395 tcaagatattcgaacagcagcgagaaatcttcaagaagcatgataaaacgcgaca 454  
QY 556 tgacagtgagcagtaagtaatgagagactacttcttattatccctgttaagacatcg 615  
DB 455 tgacctgcagctggaacgaggtgagagactaccactctccaccgcggaacacatcc 514  
QY 616 aggaatataccgttcttgaacaacttcaagaaatgacatgacataggaggaacttaacta 675  
DB 515 ccgagatcatctctacttgaagcattccagcatcttgaatggtgagaaacttaacg 574  
QY 676 ttccagatgaattcaggaagacgaaaaaattccggaatggtgaggaagcgttttg 735  
DB 575 tcccgatgagttcacagatgagagaggaagcagacggtggtggaacacacttgg 634  
QY 736 cagagagcatctgtgtgtgtctctcgacaagcactcccttggagcccttgaana 795  
DB 635 cagagaggttggtggcgcgtatccagaactgcacgcccccccgagcaggttcaag 694  
QY 796 tcatgatcaggttcaacggttcaaaatcagacaataatgaatattggtggtcttcag 855  
DB 695 tgcctatgcaaggtccatgctcccgagacaacatgagcactggtgtggtccttcaac 754  
QY 856 agatgttaaaaagaagaggtatccgtctgttggaggggaatggttaaaacgttca 915

DB 755 agatgattcgaagaagaggccaggttcaactcttggcggggaattgacaaacttca 814  
QY 916 aattgtctcttgaagacgtgttaatttggcgatataaagactagaagaagttactta 975  
DB 815 aaattgccccgaatcagacatcaaatctcatgtgctatgagacagatcaagcgttgt 874  
QY 976 ctgaagaaggaacaaaataggaacattgagaatttattctgttccatgctgag 1035  
DB 875 gtagtgaccagagactctgagatttcaagagagcttggcagggctcttggcaggg 934  
QY 1036 caactgcaagactttatatatccaatgaggttataaagacagcgtgttgaagca 1095  
DB 935 ccattgcacagagcagcatctaacatgaggttccctgaagaccggatgagcgtgcg 994  
QY 1096 aactgggagactctgtgataatagattgtgccaagaagaattttgaaacatgaagct 1155  
DB 995 agacagggccagtaactcagaatgactgagactgccaagagatctctggccaagagg 1054  
QY 1156 tggagcttttacaaggctatgttccaatttattaglatcacactatgacagca 1215  
DB 1055 tggcgccttctacaagaagctatgtcccaacatgctggcactatcccttatgcgca 1114  
QY 1216 tagatctgtgtgtatgagccttgaagctccattgtgctgataatttggaaaagt 1275  
DB 1115 tgaacttgcagtlcaagagacgtccaagaatgctgtgctgacagactatgacatga 1174  
QY 1276 ctgtaaccttgagatcagtgctgtgtgga tgcggtgctctatccatccagacactgtg 1335  
DB 1175 ggcgcgaccccgsgtltgtgtctctgctgctgctgtggacacatgtccagttactgtg 1234  
QY 1336 agctgacagctaccatctgcttgggtgagaaactgcagctcagagctcaacatgttag 1395  
DB 1235 agctgcagcagtaaccctgcctgcttagcagaccgagctgaaggcgcagactatag 1294  
QY 1396 aaggttccccacagctgtaatatggtgtgctcttccagaaatttcccaagaagga 1455  
DB 1295 agggcgtctcggaggtgacatgagcagacgtcttcaaaatactccgcggacagagg 1354  
QY 1456 taccaggaacttcaagagacatcacccaaacttcatgaaagtgtccctgtgtagca 1515  
DB 1355 ccttcgggtgttaacaggggcgtgcgcccaacttcatgaagttccacagtgtagca 1414  
QY 1516 tcagtatgtgttatgaaatatgaaatgaaacaaactttagagt 1558  
DB 1415 tcagtacgtgtgtctacgagaacctgaagatcaccttggcgt 1457  
RESULT 11  
ID AAF44204 standard; cDNA; 3334 BP.  
XX  
XX AAF44204;  
AC  
XX  
XX 02-APR-2001 (first entry)  
DT  
XX  
XX Human PRO1106 (UNQ549) nucleotide sequence SEQ ID NO:288.  
DE  
XX  
XX Human; secreted and transmembrane protein; PRO; cytoslastic;  
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
KW diagnostic assay; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200073454-A1.  
PN  
XX  
XX 07-DEC-2000.  
PD  
XX  
XX 30-MAR-2000; 2000MO-US08439.  
PF  
XX  
XX 02-JUN-1999; 99MO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 07-JUL-1999; 99US-0143048.



PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 17-AUG-1999; 99US-0149386.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 08-OCT-1999; 99US-0158663.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.

(GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
PI Grimaud CJ, Gurney AL, Kijavich IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;

DR WPI: 2001-032160/04.  
P-PSDB: AAB65241.

PT PRO polynucleotides used to produce polypeptides used to target  
PT bioactive molecules such as toxins, radiolabels or antibodies, to  
PT specific cells, to cause targeted cell death -

XX PS Claim 2; Fig 205; 935pp; English.

CC The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
CC can be used for targeted delivery of bioactive molecules, such as  
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
CC and DNA. They may also be used to produce transgenic animals which are  
CC used to develop and screen therapeutically useful reagents. The PRO  
CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.

XX Sequence 3334 BP; 788 A; 848 C; 983 G; 715 T; 0 other;

Query Match 20.3%; Score 543.8; DB 22; Length 3334;  
Best Local Similarity 64.8%; Pred. NO. 4.1e-112;  
Matches 806; Conservative 0; Mismatches 437; Indels 0; Gaps 0;

QY 316 agggagaaatttctactctgagatgtcacaagaatgggaagctgatttgaagaat 375  
DB 215 agcggaatattgtacaagctgtgagataagcactgtgagcagctacatttgaagaat 274  
QY 376 ttatgaacttaacttaagaacatgagaagaatgaatgtgcatltagaattagaaca 435  
DB 275 ttgtcatatcatcocaagatcatgagaagcgtgagcgtgtgtttagaatttggaca 334  
QY 436 aaaaatgatgaaaatattgagcctcaagaatgtccagtcctccagaacttggctc 495  
DB 335 aaaagaatgatgacgcattgacgcgcagagatcatgcatcctccctggagacttggag 394

QY 496 tgactattctgaacaacaagcagagttgattcttcaagaatgatgttgaagaca 555  
DB 395 tcaagatatctgaacaagcagcagagaataattctcaagacgttgtataaaagcagaca 454  
QY 556 tgacagtgagctgaatgaatgagagagacttacttatttaacctgttacaagacttg 615  
DB 455 tgaccatgcactgagcagcagtgagagacttaccactctccaccctccgcygaataacc 514  
QY 616 aggaataatccgttcttggaacattctacaggaattgacttaagggaataacttaacta 675  
DB 515 ccgagatcatcctcactcctgaagcatctcacaagcatctgtgtgtggaatcacaag 574  
QY 676 ttccagatgaattcaccggaacggaataaaatcccgacaatggtgtggagcgacttttg 735  
DB 575 tcccggaatgattcacaatctgagagagagcagacgggagatgtgtgtgagacactgttg 634  
QY 736 caggaagcatttctgtctgtctctcgaacaagcactgcccctttgacccgtctgaanaa 795  
DB 635 caggaggtgtggcagggcggtatccagaactcgaacgcccccttgacagcagctcaagg 694  
QY 796 tcaatgacaggttcaaggttcaaaatcagaacaaatgaacatattgtgtcttcgac 855  
DB 695 tgcctatgcaagctcactcctcccgacgaacaacatggtgcatcgtgtgtgtcctcactc 754  
QY 856 agatgttaaagaagaggtatccgcctgccttggagggaaatgtgtacaacgtcatca 915  
DB 755 agatgtatcgaagaagagggccaggttcaactctgtcggggcaatggtacacgtccctca 814  
QY 916 aaattgtctcttgagaacagctgtttaaattctcgtgacatagaaacgtacaagaattacta 975  
DB 815 aaattgcccccgatcagcatcacaatcattcattgactatgagagatcaagcgtgtgtg 874  
QY 976 ctgaagaaggaacaaataggaacatttgaagaattattctgttccatcagcttgag 1035  
DB 875 gtatgacacaggaagcctctgaagattcagcagaagcgtgtgtgcaaggtccttgaggg 934  
QY 1036 caactgcacagacttlatatccatgagaggttatgaaacagcagcgtgtgtgagca 1095  
DB 935 ccattgcgccagagcagcatctcacaatggaaggtcctgaaagcccgagatgctgtgcgga 994  
QY 1096 aaactgagcagctactctgaatatatgattgtgcacaagaagaatttgaacaatgaagct 1155  
DB 995 agacagcgcagactcagaatgactgtgactgtgcagagagatcctgtgcagagaagggg 1054  
QY 1156 tggagccttttacaagaagctatgttcccaattattagatataactatcagagca 1215  
DB 1055 tggccgcttctacaagaagctatgtcccaacatgtgtgcatcatccctatgtccgga 1114  
QY 1216 tagacttgctgtgatgagctcttgaagctcctatgtgctgataatttgcagaagaat 1275  
DB 1115 tgaacttgcaatctcagaagagcgtcacaagaatgctgtgctgagacatctgagfagaaca 1174  
QY 1276 ctgtaaacccttgagctatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1335  
DB 1175 ggcgcgaccocggcggt 1234  
QY 1336 agcttgccagctaccatctgt 1395  
DB 1235 agcttgccagctaccatctgt 1294  
QY 1396 aaggtccccaagcgtgatgattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1455  
DB 1295 agggcgctccggaggtgtgacatgagcagccttcaaacatctcctgtcggaacgggggg 1354  
QY 1456 taccaggaacttcaagagcgtacacccaacatcaatgaaggtgtcctcgtgtgtgtgtgt 1515  
DB 1355 ccttcgggctgtgacagggggcgtgcgcccaactcatgaaggtcatcccaagctgtgagca 1414  
QY 1516 tcaattatgtgtgttataataataatgaagcgaactttgagat 1558  
DB 1415 tcaattatgtgtgttataataataatgaagcgaactttgagat 1457

RESULT 12  
AAK53194  
ID AAK53194 standard; cDNA; 549 BP.  
XX  
XX AAK53194;  
XX  
XX 06-NOV-2001 (first entry)  
DE Human polynucleotide SEQ ID NO 2723.  
XX  
XX  
KW Human: cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation; ss.  
XX  
XX Homo sapiens.  
PN WO200157190-A2.  
PD  
PD 09-AUG-2001.  
PF  
PF 05-FEB-2001; 2001WO-US04098.  
XX  
XX 03-FEB-2000; 2000US-0496914.  
PR 27-APR-2000; 2000US-0560875.  
PR 20-JUN-2000; 2000US-0598075.  
PR 19-JUL-2000; 2000US-0620325.  
PR 01-SEP-2000; 2000US-0654936.  
PR 15-SEP-2000; 2000US-0663561.  
PR 20-OCT-2000; 2000US-0693325.  
PR 30-NOV-2000; 2000US-0728422.  
XX  
XX (HYSE-) HYSEQ INC.  
PI Tang YT, Liu C, Drmanac RR, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
PI Zhao QA, Wang D, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R.  
XX  
XX WPI; 2001-476283/51.  
DR P-PSDB; AAM80061.  
XX  
XX Nucleic acids encoding polypeptides with cytokine-like activities,  
PT useful in diagnosis and gene therapy -  
XX  
XX Claim 1; Page 4947; 6221pp; English.  
XX  
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activity/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation.  
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
CC (AAM80020) are omitted as the relevant pages from the sequence listing  
CC were missing at the time of publication.  
XX  
XX Sequence 549 BP; 146 A; 122 C; 152 G; 129 T; 0 other;

Query Match 20.2%; Score 540.2; DB 22; Length 549;  
Best Local Similarity 99.4%; Pred. No. 1.2e-111;  
Matches 542; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 86 gccctcgatctccgctgactctcctcgccagcgccgctcgctctgagaccatgttgcg 145  
+ |||||||  
Db 5 gtctcgatctccgctgactctcctcgccagcgccgctcgctctgagaccatgttgcg 64  
+ |||||||

QY 146 ctgctcgcgagactctcgctgctgccacgcgcgctgctcagcagcgcgagcagcgcg 205  
+ |||||||

Db 65 |||||||  
ctgctcgcgagactctcgctgctgccacgcgcgctcctcagcagcgcgagcgcgagctgcg 124  
QY 206 ctacgagaccctcttcacgacactggaaccgcaatgaggagagtggtgacatcgca 265  
+ |||||||  
Db 125 ctacgagaccctcttcacgacactggaaccgcaatgaggagagtggtgacatcgca 184  
+ |||||||  
QY 266 gctcgagagggctcaggaacctggcaccctctggccagacgcgcgagagaat 325  
+ |||||||  
Db 185 gctcgagagggctcaggaacctggcaccctctggccagacgcgcgagagaat 244  
+ |||||||  
QY 326 ttctactctggagatgtaacaaatggaagctggtatttgaagaatttgaagta 385  
+ |||||||  
Db 245 ttctactctggagatgtaacaaatggaagctggtatttgaagaatttgaagta 304  
+ |||||||  
QY 386 ccttaagaccatgataagaatggaatggtcatttaagatttgaacaaataatga 445  
+ |||||||  
Db 305 ccttaagaccatgataagaatggaatggtcatttaagatttgaacaaataatga 364  
+ |||||||  
QY 446 tggaaaattgaggtctcagaaatgtlccagctctccacagacatggtctgacttcc 505  
+ |||||||  
Db 365 tggaaaattgaggtctcagaaatgtlccagctctccacagacatggtctgacttcc 424  
+ |||||||  
QY 506 tgaacacacagcagagttgattcttcaagcattgattgtatggagacaaatgacatga 565  
+ |||||||  
Db 425 tgaacacacagcagagttgattcttcaagcattgattgtatggagacaaatgacatga 484  
+ |||||||  
QY 566 ctggaatgaatgagagactctcttatttaacctgtacagacatgagagaattat 625  
+ |||||||  
Db 485 ctggaatgaatgagagactctcttatttaacctgtgtacagacaaatgagagaattat 544  
+ |||||||  
QY 626 ccgctt 630  
+ |||||  
Db 545 ccgctt 549

RESULT 13  
AAS44597  
ID AAS44597 standard; DNA; 2625 BP.  
XX  
XX AAS44597;  
AC  
AC 18-DEC-2001 (first entry)  
XX  
XX Human full-length polynucleotide sequence #22.  
DE  
DE  
XX Mammal: human; rhesus monkey; baker's yeast; fission yeast; Norway rat;  
KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;  
KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;  
KW nervous system disorder; inflammatory disorder; cell differentiation; ds;  
KW anglogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;  
KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;  
KW cytotoxic; antineoplastic; antitumor; antitumor; antitumor; antitumor;  
KW antibacterial; immunosuppressive; vasculitic; antiparkinsonian;  
KW neuroprotective; osteoporotic; antidiabetic; antidiabetic; antidiabetic;  
KW immunostimulant; analgesic; gene therapy.  
XX  
XX Homo sapiens.  
OS  
OS  
XX MO200164834-A2.  
PN  
PN  
XX 07-SEP-2001.  
PD  
PD  
XX 26-FEB-2001; 2001WO-US04926.  
PF  
PF  
XX 28-FEB-2000; 2000US-0515126.  
PR 18-MAY-2000; 2000US-0577409.  
PR 17-JUN-2000; 2000US-0597707.  
PR 14-JUL-2000; 2000US-0616807.  
PR 19-SEP-2000; 2000US-0664641.  
XX  
XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F, Xu C;  
PI Xue A, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;  
PI Dmanac R;  
XX  
DR WPI: 2001-589862/66.  
XX P-PSDB: AAU27697.  
DR  
XX  
XX Novel polypeptides and nucleic acids obtained from cDNA libraries  
PT prepared from various human tissues, for diagnosis, treatment of  
PT cancer, neurological, inflammatory disorders and for use in arrays for  
PT detection -  
XX  
PS Claim 1; SEQ ID NO 22; 153bp; English.

Sequence: AAS44576-AAS44919 represent full-length polynucleotides and  
conting polynucleotides encoding polypeptides of the invention. The DNA  
and protein sequences are useful for the treatment, diagnosis and  
prevention of various types of disorder in a mammalian subject such as a  
human, dog, monkey, mouse, hamster or rat. The disorders include cancers  
such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such  
as multiple sclerosis, connective tissue disease, rheumatoid arthritis,  
diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system  
disorders such as Parkinson's disease, Alzheimer's disease, Huntington's  
chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and  
Wernicke disease, inflammatory disorders such as nephritis, Crohn's  
disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory  
bowel disease. The sequences exhibit activity relating to angiogenesis,  
cell proliferation, cell differentiation, stem cell growth factor,  
activin or inhibin. Therefore, they can be used to manipulate stem  
cells in culture to give rise to neuroepithelial cells that can be used to  
augment or replace cells damaged by illness, accidental damage or genetic  
disorders. The sequences may also be used for regeneration of bone,  
cartilage, tendons and ligaments and in tissue repair and burn healing.  
Note: Some sequences for this patent did not form part of the printed  
specification, but were obtained in electronic format directly from WIPO  
at ftp.wipo.int/pub/published\_pcl\_sequences.

Query Match	20.0%;	Score 534.2;	DB 22;	Length 2625;
Best Local Similarity	61.9%;	Pred. No. 5.4e-110;		
Matches 864;	Conservative 0;	Mismatches 528;	Indels 3;	Gaps 1;

[illegible]

D	b	552	ctggaaaatg	gggagcg	tgctgtat	ttcttggaa	gcatccacg	gtccttgacat	gtgc	611																	
Q	y	663	gatagctta	actatctcca	gatagta	ttcaacg	gaagacg	aaaaaaatcc	gcgacata	tg	722																
D	b	612	gagtcctga	acagatgc	ccggacga	gttctcca	aaagaaga	gactgac	ggcgat	tg	671																
Q	y	723	aggaagctt	tggaagga	gagatgtgc	gtgcgtct	ctcttcg	aaacgaac	gacatgc	cttc	782																
D	b	672	aaacgcctg	ggtg	ccggccg	caggtgc	gagctgt	ccaagga	gcagccg	ccctc	731																
Q	y	783	gacgcctga	aaatccat	gata	tgcaagtt	ctacggtctt	caaaatcc	aaagacaaat	gtgacatat	842																
D	b	732	gaccgcctc	aaaggtct	cttcacat	gagtgccat	gactcaag	aagacac	ccggctg	taacatcc	791																
Q	y	843	gggtgcctt	cgacaga	tgtgtaaa	agaagagat	ctccgtc	gtcttgg	aggggaat	gtc	902																
D	b	792	ggggggctt	cgaaagac	tggtctct	gtgaagg	gagcatcc	gtccctgt	ggcgcg	caat	851																
Q	y	903	acaaacg	ctacaat	ttgctctcc	ggagacgc	gctttaa	ctctgggc	catatga	acagtc	962																
D	b	852	atatagt	ctaccaa	gatgtgc	cccgagtc	gcatcat	caagttca	gtgctct	atgaacagatc	911																
Q	y	963	aagaag	tactact	gtgaaga	gagcaaaaa	atagaaca	tttgag	agattat	ctctgt	1022																
D	b	912	aagaggg	ccatcc	ctggcg	cagcag	gagacat	gctatgt	gaagga	ggtctc	gtgc	971															
Q	y	1023	tcctatg	ctggaag	caactgc	acagac	cttata	ttatcca	atgaggt	ttatga	aac	cg	108														
D	b	972	tcctcgg	ctctgtgc	acaagcc	aaacaa	ccatatt	ccatctat	gtgaag	tgctgta	aga	cg	103														
Q	y	1083	ctggctg	taaggca	aaatctgg	cgatc	ctcgg	ataata	tgatgt	gtcc	aaaga	aa	tt	g	114												
D	b	1032	ctgac	cttgcg	ccggag	cggcgac	gtatga	gggctg	ctgac	tcg	cgccag	g	ctatcc	g	109												
Q	y	1143	aaacatga	aggcttg	gagac	cttttaca	aaagctat	gttcc	aatattat	agat	at	cat	a	120													
D	b	1092	gaga	ggagag	ggcccg	tgctctt	ctac	cggtg	tac	ctcc	aaacgt	g	ctgtg	cat	c	115											
Q	y	1203	ccctat	cgacga	catagat	ctctgc	ctgtga	gagctct	tgaa	ctccat	gtatg	gtgc	tg	at	126												
D	b	1152	ccctat	gcgg	catcgac	gcac	ctggcc	gtctta	cga	gactct	gtga	aaatct	gtg	gtc	ta	ca	g	121									
Q	y	1263	tttg	caaa	aga	attctgt	aaac	ccctgt	ga	gtcat	gtgtg	ctg	ggag	ab	cg	gt	cc	ta	cc	132							
D	b	1212	tac	agcca	gca	gtc	gcagac	ccca	ggcat	cc	ctc	gtc	ctc	gt	cg	ta	ccat	cc	127								
Q	y	1323	agac	ccgtgt	gta	gcg	gcgc	gac	gac	ctcc	atg	gtc	gttg	ga	ga	act	tc	ga	tg	aa	g	138					
D	b	1272	agcc	cccg	ggccga	ga	aaac	agat	ctac	ccg	ctgtg	cc	ctg	ga	gc	ga	cc	gc	ga	gc	ga	133					
Q	y	1383	caaa	gcata	gttga	aa	ggcttcc	ccca	gcgct	gt	aaat	atgt	gtgc	ctc	ctt	tc	ga	ac	ga	att	144						
D	b	1332	caag	ctcc	atc	gat	gggtg	cc	ccca	gt	ctc	at	gt	g	ct	ga	ct	aa	ct	cc	139						
Q	y	1443	tc	caaa	aa	ga	gaata	cca	gga	ctt	at	ca	ga	g	cat	ca	cc	cc	aa	act	ta	ga	ag	gt	ctc	150	
D	b	1392	tc	ca	ga	ga	ga	g	at	g	at	g	at	g	at	g	at	g	at	g	at	g	at	g	at	145	
Q	y	1503	cc	ct	ct	ta	ga	cat	ca	gt	tt	gt	gt	tt	ta	ga	aa	ta	ga	aa	ca	act	ta	ga	gt	aa	156
D	b	1452	cc	ga	ct	gt	tg	ga	cat	ct	cc	ct	at	gt	gt	ct	aa	ga	aa	ca	ta	ga	aa	ca	g	ct	151
Q	y	1563	caga	aat	ga	t	ga	t	gt	gtc	1577																
D	b	1512	tc	ca	ga	at	cc	ct	ct	gtc	1526			</													

```

RESULT 14
AAS44769
ID AAS44769 standard; DNA; 2644 BP.
XX
AC AAS44769:

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XX 18-DEC-2001 (first entry)  
DT  
XX  
DE Human contig polynucleotide sequence #22.  
XX  
KW Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;  
KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukemia;  
KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;  
KW nervous system disorder; inflammatory disorder; cell differentiation; ds;  
KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;  
KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;  
KW cytoskeletal; antirheumatic; antiarthritic; vulnery; antiinflammatory;  
KW antibacterial; immunosuppressive; vasotropic; antiparkinsonian;  
KW neuroprotective; osteopathic; antidiabetic; antistimulant; antiallergic;  
KW immunostimulant; analgesic; gene therapy.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200164834-A2.  
XX  
PD 07-SEP-2001.  
XX  
PF 26-FEB-2001; 2001WO-US04926.  
XX  
PR 28-FEB-2000; 2000US-0515126.  
PR 18-MAY-2000; 2000US-0577409.  
PR 17-JUN-2000; 2000US-0597707.  
PR 14-JUL-2000; 2000US-0616807.  
PR 19-SEP-2000; 2000US-0664641.  
XX  
PA (HXSE-) HXSEQ INC.  
XX  
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
PI Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;  
PI Dmanac R;  
XX  
DR WPI: 2001-589862/66.  
DR P-PSDB; AA027869.  
XX  
PT Novel polypeptides and nucleic acids obtained from cDNA libraries  
PT prepared from various human tissues, for diagnosis, treatment of  
PT cancer, neurological, inflammatory disorders and for use in arrays for  
PT detection -  
XX  
PS Claim 1; SEQ ID NO 366; 153bp; English.  
XX  
CC Sequences AAS44576-AAS44919 represent full-length polynucleotides and  
CC contig polynucleotides encoding polypeptides of the invention. The DNA  
CC and protein sequences are useful for the treatment, diagnosis and  
CC prevention of various types of disorder in a mammalian subject such as a  
CC human, dog, monkey, mouse, hamster or rat. The disorders include cancers  
CC such as leukemia, lymphoma and neuroblastoma, autoimmune disorders such  
CC as multiple sclerosis, connective tissue disease, rheumatoid arthritis,  
CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system  
CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's  
CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and  
CC Wernicke disease, inflammatory disorders such as nephritis, Crohn's  
CC disease, ischemia-reperfusion injury, shock, sepsis and inflammatory  
CC bowel disease. The sequences exhibit activity relating to angiogenesis,  
CC cell proliferation, cell differentiation, stem cell growth factor,  
CC activin or inhibin. Therefore, they can be used to manipulate stem cells  
CC in culture to give rise to neuroepithelial cells that can be used to  
CC augment or replace cells damaged by illness, accidental damage or genetic  
CC disorders. The sequences may also be used for regeneration of bone,  
CC cartilage, tendons and ligaments and in tissue repair and burn healing.  
CC Note: Some sequences for this patent did not form part of the printed  
CC specification, but were obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 2644 BP; 568 A; 825 C; 743 G; 508 T; 0 other;

Query Match		20.0%;	Score 534.2;	DB 22;	Length 2644;
Best Local Similarity		61.9%;	Pred. No. 5.4e-110;		
Matches 864;		Conservative 0;	Mismatches 528;	Indels 3;	Gaps 1;
Oy	186	gacgcgagcagccgacgcagctacagaccctctccagcgacgtgcacgcagctggagac	245		
Db	133	gaccgcgagcgccgagcgagcgctgctgctgtctgagcgagcgctggacaagaagat	192		
Oy	246	ggaagtgtgacatcgcgcagctgcaggaaggcgctcaggaacctgggc--atccctctg	302		
Db	193	ggccgcgtggagcgcgcagagatgctgcagagggctggccagcctgggcgagggacaacca	252		
Oy	303	ggccagagcgcgcgcgggggaaatttttactctgtgagatgcacaaagatggagacgtg	362		
Db	253	gaccccgccgcccaacagggatctctctctgagggtgatgtgcaccagatggcgggcct	312		
Oy	363	gatttgaagaattatgaattacctaagaacacatgagaagaatgaaattggacatt	422		
Db	313	gacctggaggaatttcccgctatctgcagagcgaggacaacgcgtctgctgtcattgtt	372		
Oy	423	aagaattgacaaaataatgatgaaaattgagccttcagaataatgtccagctctc	482		
Db	373	cacagcttgaccgcgaaccagatgctacatgtatgtctctgagatccacaagaatttc	432		
Oy	483	cagacactgggtctgactatttctgaaacaaacagacagatgtattcttcaaaagatgat	542		
Db	433	cgagctcgggcattctccatctcgtgagcagggctgagaaatttgcacaagatggac	492		
Oy	543	gttatggacacatgacagtgactgagatgaatgagagactacttcttaattactc	602		
Db	493	cgagacgycacaatgaccatgtgactgcaagaatggcgacacactcttcgttgcattcg	552		
Oy	603	gtacagacatttggaaatataccgttcttcgaaacattctacagaattgacatggg	662		
Db	553	ctggaaaatgtggagacgtgtgattcttcggaagcattccacgltccgtgacatggc	612		
Oy	663	gatagcttaactatccagatgaattccaggaacgaaagaaataatccggacaattgttg	722		
Db	613	gagtgcctgacagtgccgcgagatctccaaagacagagctgcagggacatgtgtggg	672		
Oy	723	agcgacgttctggcagagggcagtgctgtgtctctcgaacaacgacgtccctcttg	782		
Db	673	aaacgctggtggccggcgagtgtaggtgctgtcgtgtacgagacagggacggccctctg	732		
Oy	783	gaccgtcgaataatcatgatgacaggttcaacggttccaaatcaagacaaaatgaacatat	842		
Db	733	gaccgctcgaaggtcttcatgacgttccatgcattcaagacaaacggctgtgaacatcct	792		
Oy	843	gttgcttgcagcagatgtgaaagaaggaggtatccgctcgttggaggggaaatggt	902		
Db	793	gggggcttcgaagcatggtctctgaggaggacatccgctcctctgtggcggcaatggt	852		
Oy	903	acaaacgtcatcaaatgtctctctgagacagctgttcaattctggtgacatgacagtc	962		
Db	853	attaatgaccacaagatgtgcccccgagtcagctalcaatgttcgtcctatgacagctc	912		
Oy	963	aagaatgtaactactgaaagaagacaataaataaggacaattggagagattattctggt	1022		
Db	913	aagagggccatctcgtggcgacagagagacactgcatgtgcagggcgcttctgtgctggc	972		
Oy	1023	tcacatgcttgagcaacatgcacgcacagactttatatccatgaggggtatgaaacccgg	1082		
Db	973	tcacctgtgtgtgcacacggcccaacacatcatcttaacctatggaggtgtcgtgaaagcgg	1032		
Oy	1083	ctggctgtgagcacaactggtgcagctactctggaatatagtattgtgcacaagaatattg	1142		
Db	1033	ctgacctggcgcgcgagcgagctacataaagggtgcgtgcgtcgcgcagagcgatcctg	1092		
Oy	1143	aaacatgaaagcttggagcctttttacaagagctatgttcccaatttatatgtatcata	1202		
Db	1093	gagagggaggggcccgcgtctcttcaacgcggtacacccccaacgltgttggacatc	1152		
Oy	1203	cctatgacggcatagatcttgcgtgtgtatgagctccttgaagctctatgtgctgataat	1262		

Db 1153 ccctatgctgggcatgcagctgcgcgtctacgagactctgaagactctgtgtcttcagcag 1212  
QY 1263 ttgtcaaaagatctcttaaacctctgaagtcagtgtctgtggagcgggtccctatcc 1322  
Db 1213 taagcagcagctcgcgcagccagcagcatcctcgtctcctgtgcgtgcgttaccatctcc 1272  
QY 1323 agcacctgtgtcagctgcgcagcactaccatctgtgtctgtgaagactcgcagcagct 1382  
Db 1273 agcacctgtgcgcagcagatgacgacttaaccgctgtgcccctgtctccgagccagcagcag 1332  
QY 1383 caagcagatgttagaaggttcccccacagctgaataatgtgtgctcctcttcgcagcaatatt 1442  
Db 1333 caagcctccatcgagggtgtgcgcccaagctgtccatgtcgtgtcgtcagctacatccctg 1392  
QY 1443 tccaaagaagaataccaggaactttaagaagagcgtaccccccaactctatgaagggtc 1502  
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Db 1453 ccagcgtgtgagctctcctctatgtgtgtctacgagaacatgaagcagccttggggttcag 1512  
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Db 1513 tccagatcctcttcg 1527

## RESULT 15

AAC76538  
ID AAC76538 standard; cDNA; 1481 BP.

XX AAC76538;

XX 08-FEB-2001 (first entry)

XX Human ORFX ORF2093 polynucleotide sequence SEQ ID NO:4185.

XX Human: open reading frame; ORFX: detection; cytostatic; hepatotropic;  
XX vulnerrary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;  
XX anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
XX immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
XX hypotensive; dermatological; immunosuppressive; antineoplastic;  
XX antiviral; antibacterial; antifungal; antineoplastic; antihypertensive;  
XX antianemic; gene therapy; cancer; proliferative disorder; hypertension;  
XX neurodegenerative disorder; osteoarthritis; graft vs host disease;  
XX cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
XX cholesterol ester storage; systemic lupus erythematosus; infection;  
XX severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
XX allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
XX bone damage; cartilage damage; antiinflammatory disease; coagulation;  
XX thrombosis; contraceptive; ss.

XX Homo sapiens.

XX WO200058473-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US08621.

XX 31-MAR-1999; 99US-0127607.

XX 02-APR-1999; 99US-0127636.

XX 05-APR-1999; 99US-0127728.

XX 30-MAR-2000; 2000US-0540763.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI: 2000-602362/57.

XX P-PsDB; AAB42329.

PT Novel nucleic acids and peptides derived from open reading frame X,  
PT useful for treating e.g. cancers, proliferative disorders,  
PT neurodegenerative disorders and cardiovascular disease -  
PS Claim 5; Page 3377-3378; 5507P; English.

CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
CC sequences have activities such as: cytostatic; hepatotropic; vulnerrary;  
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;  
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;  
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;  
CC antidiabetic; hypotensive; dermatological; immunosuppressive;  
CC antineoplastic; antibacterial; antiviral; antifungal; antineoplastic;  
CC antihypertensive; antianemic. The sequences can be used for determining  
CC the presence of or predisposition to, or preventing or treating  
CC pathological conditions associated with an ORFX-associated disorder. The  
CC nucleic acids can be used to express ORFX proteins in gene therapy  
CC vectors. The proteins and nucleic acids may be used to treat cancers,  
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance  
CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 1481 BP; 331 A; 411 C; 465 G; 273 T; 1 other;

## Query Match

18.5%; Score 494.4; DB 21; Length 1481;

Best Local Similarity 64.5%; Pred. No. 3.7e-101;

Matches 738; Conservative 0; Mismatches 406; Indels 0; Gaps 0;

QY 415 tggcatttaagaagtttagcaaaataatgaagaaatgaagcttcgaagtctcc 474  
Db 2 tgggttttaagagtttgacaaaagaatgatgagcatttgagcgcagagatcagtc 61  
QY 475 agtctctcagacactggtctgaactattcttcgaacaagcagagtgattcttcaaa 534  
Db 62 agtccctcgagcgttggtgagatcagatctcgaacagcagcgaaataattctcaaga 121  
QY 535 gcttgaatgttgtaggaagatgacagtcagtcaggaatgtagagagactctctat 594  
Db 122 gcatgataaagcagcagatgacacatgcagtcgagcagtgtagagactacaccc 181  
QY 595 ttaatcctgttaacagacattgagaaattatccgttcttgaaacattctacagaaattg 654  
Db 182 tcaaccccgtagaataacatcccgagatcctcctacttggaagcattccacgtcttg 241  
QY 655 acataaggagatagacttaactatccagatgaattcagcgaagcgaataaatccgac 714  
Db 242 atgtgttgagaaatctacagctcccgatgattcagatgtagagagcagcgaggga 301  
QY 715 aatgtgtgagcagcgttcttgaggaagcattctgtgtgtctctcgaacaagcagctg 774  
Db 302 tgtgtgtgagacacctgtgtgcaggaagtggtggtggtggtggtggtggtggtggtggt 361  
QY 775 ccccttggacgctctgaataatcatgtatgcaggttccaggttcaaaaatcagcaaaaatga 834  
Db 362 ccccccgtgagcagcgtcaagtggtctcatgagtcacgtctcccggaacaacaatg 421  
QY 835 acataattgtgtcttcgaacagatgtgtaaaagagaggtatccgctcgtcttgaggg 894  
Db 422 gcatcgtgtgtgtcttactacagatgttcgaagaaggtggtggtggtggtggtggtggtggt 481  
QY 895 gaatgtacaacagcgtacataaatgtctctcagagacgtgttaattcttgagcagatg 954  
Db 482 gcaatgtgacacagcgtccctcaaaaatgtcccggaatcagcattcaaaatctatggtccatg 541  
QY 955 aacagtaacaagtaacttactgaagaagcgaataaataagaaacattgagagattat 1014



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2002, 03:16:39 ; Search time 64.41 Seconds  
(Without alignments)  
10193.733 Million cell updates/sec

Title: US-09-777-921A-1  
Perfect score: 2673  
Sequence: 1 ccgcaaccccgagcgccgcccc.....ataccatgcatgattctg 2673

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Issued\_Patents\_NA:\*  
1: /cgn2\_6/prodata/1/ina/5A.COMB.seq:\*  
2: /cgn2\_6/prodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/prodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/prodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/PCrUS.COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	545.4	20.4	1816	3	US-09-188-930-262 Sequence 262, App
2	337.2	12.6	997	3	US-09-188-930-23 Sequence 23, Appl
3	86	3.2	437	4	US-08-905-223-87 Sequence 87, Appl
4	55.8	2.1	7218	1	US-08-232-463-14 Sequence 14, Appl
5	53	2.0	19124	2	US-08-487-8268-13 Sequence 13, Appl
6	52.8	2.0	2447	2	US-09-014-969-14 Sequence 14, Appl
7	52.2	2.0	3852	1	US-07-867-106-2 Sequence 2, Appl
8	50.6	1.9	1117	4	US-09-247-3738-33 Sequence 33, Appl
9	50.4	1.9	3138	1	US-07-867-106-4 Sequence 4, Appl
10	50	1.9	19124	2	US-08-487-8268-13 Sequence 13, Appl
11	49.8	1.9	1667	1	US-08-485-284A-1 Sequence 1, Appl
12	49.6	1.9	2064	1	US-08-343-428-1 Sequence 1, Appl
13	49.2	1.8	636	4	US-08-998-416-1137 Sequence 1137, Ap
14	48	1.8	8438	1	US-07-945-283-1 Sequence 1, Appl
15	47	1.8	615	4	US-08-998-416-186 Sequence 186, App
16	47	1.8	1402	1	US-08-447-965A-1 Sequence 1, Appl
17	46.6	1.7	6243	2	US-09-056-075-1 Sequence 1, Appl
18	45.8	1.7	1441	4	US-08-821-894-63 Sequence 63, Appl
19	45.6	1.7	837	4	US-08-998-416-288 Sequence 288, App
20	45.4	1.7	240	1	US-08-628-417-6 Sequence 6, Appl
21	45.2	1.7	688	4	US-08-998-416-972 Sequence 972, App
22	45.2	1.7	1311	4	US-09-068-140A-9 Sequence 9, Appl
23	45.2	1.7	2621	2	US-08-553-619B-8 Sequence 8, Appl
24	45	1.7	1371	2	US-08-910-731-1 Sequence 1, Appl
25	45	1.7	1371	2	US-08-910-731-1 Sequence 1, Appl
26	45	1.7	1371	2	US-08-910-731-1 Sequence 1, Appl
27	45	1.7	5150	4	US-09-068-140A-14 Sequence 14, Appl

C	28	43.8	1.6	660	1	US-07-991-867B-32	Sequence 32, Appl
C	29	43.8	1.6	660	1	US-08-107-755A-32	Sequence 32, Appl
C	30	43.8	1.6	660	2	US-08-544-332-32	Sequence 32, Appl
C	31	43.8	1.6	1511	1	US-07-991-867B-8	Sequence 8, Appl
C	32	43.8	1.6	1511	1	US-08-107-755A-8	Sequence 8, Appl
C	33	43.8	1.6	1511	2	US-08-544-332-8	Sequence 11, Appl
C	34	43.8	1.6	4810	3	US-08-852-629-15	Sequence 15, Appl
C	35	43.8	1.6	4838	3	US-08-852-629-15	Sequence 15, Appl
C	36	43.6	1.6	1519	1	US-07-971-759-19	Sequence 14, Appl
C	37	43.6	1.6	7218	1	US-08-232-463-14	Sequence 14, Appl
C	38	43.6	1.6	8220	2	US-08-568-459A-11	Sequence 11, Appl
C	39	43.6	1.6	8220	2	US-08-487-826B-11	Sequence 12, Appl
C	40	43.4	1.6	43676	3	US-09-356-952-12	Sequence 1, Appl
C	41	43.2	1.6	906	1	US-08-100-874-1	Sequence 1, Appl
C	42	43.2	1.6	23673	4	US-09-773-816-1	Sequence 3, Appl
C	43	43	1.6	6124	4	US-08-213-419B-3	Sequence 35, Appl
C	44	42.4	1.6	1092	2	US-08-646-550B-35	Sequence 35, Appl
C	45	42.4	1.6	1092	2	US-09-412-184-35	Sequence 35, Appl

## ALIGNMENTS

RESULT 1  
US-09-188-930-262  
; Sequence 262, Application US/09188930A  
; Patent No. 6150502  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murison, James Greg  
; TITLE OF INVENTION: Compositions Isolated From Skin Cells  
; TITLE OF INVENTION: and Methods For Their Use  
; FILE REFERENCE: 11000.1011c1  
; CURRENT APPLICATION NUMBER: US/09/188,930A  
; CURRENT FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 348  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 262  
; LENGTH: 1816  
; TYPE: DNA  
; ORGANISM: Mouse  
US-09-188-930-262

Query Match 20.4%; Score 545.4; DB 3; Length 1816;  
Best Local Similarity 64.9%; Pred. No. 1.2e-130;  
Matches 807; Conservative 0; Mismatches 436; Indels 0; Gaps 0;

QY	316	aggagaaatttctactctgagatgcaacaagaatggaagctgatttgaagaat	375
DB	216	agcgaagaattgtgcaagcgtgcaagacgtgagcttgagcaactggaacttgaagt	275
QY	376	ttatgaatctctaaagaccatggaagaatggaatgtgcatcttaagaattgagca	435
DB	276	ttgtacattctcccaagatcatggaagaatggaatggaatggaatggaatggaatgga	335
QY	436	aaaataatggaagaatgtgagcttcaagaatgtgcatcttccagaaactggtc	495
DB	336	aaaagaatgagtgatcgaatgcatgagtgatgagtgatgagtgatgagtgagtgagtg	395
QY	496	tgactattctggaacaagaatggaatgtgatttctcaagaatggaatgtgattgagca	555
DB	396	tcaagatctcgaagaatggaatggaatggaatggaatggaatggaatggaatggaatgga	455
QY	556	tgaacagtgatggaatggaatggaatggaatggaatggaatggaatggaatggaatgga	615
DB	456	tgaacagtgatggaatggaatggaatggaatggaatggaatggaatggaatggaatgga	515
QY	616	aggaatattcgttcttctggaacattctacagaatggaatggaatggaatggaatgga	675

Dh	516	cggaaatcatcctctgtaactcgggaagcactctgcagaactcttcgaatgtctgaaatctgacag	575
OY	676	ttccagatgaaattcacgcgaaagacgaaanaaaatcccgagacaattggtagagacagctttgg	735
Dh	576	tcccaacatgaaattctacaaatctgaaagagacgacagcgaggatgtggtagagacacttgtag	635
OY	736	caaggagcaattgctgtagctgtctctcctgaaacaaagcattgcaccttttgagacgctcgaaaa	795
Dh	636	caaggagagcgaggcgcaaggcagattcccaagaaactctgcagctgcaccttcgaaagacatgaaag	695
OY	796	tcaatgatacaggtttcacggtttcaaaatcacagacaanaatgaaacatatttggtagctttcgac	855
Dh	696	tgctcatctgacgttccatctgcctcccgagcaacaacatgtgcatcgtatgagtgagttcaacac	755
OY	856	agatgtgtaaaagaaagagagatgtctccgctcgtcttggagaggaaatgtgtacaacgctacaa	915
Dh	756	agatgatcttcggaaagaggggaaacccaagcttaactctgtagcggggacaacggtcatcaatgtctcca	815
OY	916	aaatgtgctcccgaaacaaactgttataattcttgtagcatatgaaagctaaagaaatttactta	975
Dh	816	aaattgccccctgagctgcgacatactcaatctaatctatgtgacataatgtgacagaaacgctgtcag	875
OY	976	ctgaaagaaagcaaaaataagaaacattgtagagattatcttctggttccatgagctgtagag	1035
Dh	876	gtagtgatacagaaagaaacgctgtagagattccacagaaagccttggtagagcctctctgcccagag	935
OY	1036	caactgcacaaactttatataatccaatggtaggggttaagaaacaaagcgtgcgtctgttaga	1095
Dh	936	ccattgcccccaagtagcatctacccaattgtagaggttctctgaaagaccgaatgacgtgcccgcgga	995
OY	1096	aaactgtagcagctactctggaatataatgatgtgtgcgaagaagaatttgaacaatagaaagct	1155
Dh	996	aaacaaagaaacagtaactccgagcatgtctgtgacgtgtgcagagaaatcttgcgttaagaaggggtg	1055
OY	1156	tgggaagacttttaaaaagggcctagttcccaattatgaatgatacatttaacttgaagaa	1215
Dh	1056	tagctgctcttcaaaaagggcctaaatcccccaacatgcgtggagatcaaccccctatgctgtgga	1115
OY	1216	tagaatctgctgtatgataagcctctctgaagcctcaattgctgctgataaatttgcgaaaaagatt	1275
Dh	1116	tgcagccttagcgtctcatgagaaacttgaanaatacctgcgtccagcgctacgacgaatgaaca	1175
OY	1276	ctgtaaaacccctgagatgcatagtgtgtctgtagagtaggggtgccttatccagacactgtgtgc	1335
Dh	1176	gtgcagaagcccccgggtgtgtctgcgtccctcgtgcgtgtgatactatctccagtaattgtgtgc	1235
OY	1336	agctgcgcacagctaaccccttgcttgcttggtagaacctgcgatacgaagctcaagacatgttag	1395
Dh	1236	agctgcgcacagctaaccccttagcctctgtagggccggagctcgaagtgacaacagcttccatgt	1295
OY	1396	aaggtttcccaacagctggaataatgtgtgcgctcttcgcagcaatctatttccaagaagaa	1455
Dh	1296	agggcgcgaacttggaggttaaccatagagacgctcttccaanaagattctgtcggaacttggaggg	1355
OY	1456	taccagaaacttcaagagcatcaacccaacaaattgaagaatgtgccccttgtagtga	1515
Dh	1356	cccttgggccttaacgggggctgtagcccccaacttcaatcgtgaaggtatcccccggctgtgtgaga	1415
OY	1516	tcagtatgtgtgttatgaaataatgaagaacatttaaggagt	1558
Dh	1416	tcagctacgtgtgtctacgaaacaaacttgaagaatcaaccttgggct	1458

```

: TITLE OF INVENTION: Compositions Isolated From SK1n Cells
: TITLE OF INVENTION: and Methods For Their Use
: FILE REFERENCE: 11000.1011c1
: CURRENT APPLICATION NUMBER: US/09/188,930A
: CURRENT FILING DATE: 1998-11-09
: NUMBER OF SEQ ID NOS: 348
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO. 23
: LENGTH: 997
: TYPE: DNA
: ORGANISM: mouse
: US-09-188-930-23

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Query Match:	12.6%	Score 337.2;	DB 3;	Length 997;
Best Local Similarity	64.5%	Pred. No. 3.1e-77;		
Matches 504; Conservative	0;	Mismatches 278;	Indels 0;	Gaps 0;

QY	316	aggagaaatttctactacgtagcgagatgtcaacaaagatggaaagcgaggttttggaaagt	375
Db	216	agccgaaaataatgtctcaagcaggttgacaagaagactcttattgtgcgaactcttgaaaggt	275
QY	376	ttatgaaagtaaccttaagaagaccatgagaaagaaatgaaattgtagcatcttaagagtttgaaca	435
Db	276	ttgtacattacatcccaagtcacatgagaaaaactgagcgctggtgttccaagagatcttgaca	335
QY	436	aaaaataatgtagaaaaaatgtagggtctcagaatattgccagttctccagaacatggtctc	495
Db	336	aaaaagatgtagtgcgaatctgcatctgaagatcatctgacatctccgcgcggagacttggtg	395
QY	496	tgaatattcttgacaacaacagagagatgttgattcttcaaaagcatgtgattgtttgtagaca	555
Db	396	tcaagatctctcggaacacagcagcgagagaaagattcttaagaagcatgtagaaatgtgcaga	455
QY	556	tgcacagtgcagctgaaatgaaatggagagaaacttcttattcaatccctgtctaaagacatrg	615
Db	456	tgcaccatcgcagctgaaagagatgtgagagatactacactctctgcacactctgtgtagaacaatcc	515
QY	616	agggaattatccgcttctcttgaaaaacattctcacaggaattgacataaggagatagcttaacta	675
Db	516	cggagatcatcatccctgttacttggaaagcaactcgcagatctcttgatgtcgtgtgagaacttgcag	575
QY	676	ttccagaatgaattccaagaaagacgaaaaaaaactccgcgaacaatggttgagagcagctttgg	735
Db	576	tcccaagatggttccacacagtgtagagagaaagcgacagcgagatgtcgtgtgagagacccgtgtg	635
QY	736	cagagagcatctctgtgtcgtctctcgaacaacagcaactgcccctcttgagacgcctctgaaaa	795
Db	636	cagagagtgtaggtcagagggcagatttccagaacactgtcacctgcacccctctgcagacagatgaa	695
QY	796	taatgtatgcaggtgtcaacggtttcaaaatcagacaaataagacaatatattgtgtgcttcgac	855
Db	696	tgcctcaagcaggttccatgtcctcccgacgacaacaacatgtgcactgtgaagtgtgattccaac	755
QY	856	agaatgtgaaagaagaaaggtatccgctctgcgtcttgaggggaattgttcaaaagctgcaca	915
Db	756	agatgattctgagaaaggggagagccaagtcaactctgcgcgggagcaacggcatcattgtccctca	815
QY	916	aaattgtcctctgagacagctgttaaattctctggtacatagaaacagtacaagaagtactta	975
Db	816	aaattgcctctctgagctgcgcacataacattcatctatgagacatgaaacagcttctgtc	875
QY	976	ctgaagaagaagcaaaaaataggaacatttgagagatttatcttctgttccatagctgtgag	1035
Db	876	gtatgtatcagaggaagcgtgaagatctccacgaaaggtctgttgcaagctctcttgcgcagag	935
QY	1036	caactctcacagacatttatatatccaatgtagagttatgaaacccaggtctgtgtagaca	1095
Db	936	ccattgtcccaagtagcatctacatcccaatgtagagttctctgaagaccctgaatgctcctgtcga	995
QY	1096	aa 1097	
Db	996	aa 997	









Db 931 TAGATAATGACATCA 915

```
RESULT 9
US-07-867-106-4
; Sequence 4, Application US/07867106
; Patent No. 5389526
; GENERAL INFORMATION:
; APPLICANT: Slade, Martin B
; APPLICANT: Chang, Andy C M
; APPLICANT: Williams, Keith L
; TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
; TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526r1s
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/867,106
; FILING DATE: 19920625
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PJ 7187
; APPLICATION NUMBER: PCT/AU90/00530
; FILING DATE: 02-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Feeney, Joanne Longo
; REGISTRATION NUMBER: 35,134
; REFERENCE/DOCKET NUMBER: RICE-0002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3138 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-07-867-106-4
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Query Match 1.9%; Score 50.4; DB 1; Length 3138;
Best Local Similarity 50.4%; Pred. No. 0.004;
Matches 123; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 1846 tgaaatgactgctgaacaaattgtttgtgtgtagagttataatcataatc 1905
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1865 TTAAATAAACTGGTGGTTGTTAATTATTGAAATTTAAACCCCAATTAATAAAA 1924
QY 1906 ttcttcggggtgttcacgttttagcaggttccttatataattcttgttata 1965
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1925 AAAAATGGGATTCAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1984
QY 1966 tatitggaatgctttatagatttcttaaatctccattagaaacattagaanaatc 2025
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1985 TTTTCAGATTGCAATAAAAGATTTTTTTTTTTTTTTCTTATTCTTAACAATAA 2044
QY 2026 attcaattaaataatatactacagcaaaagcatcccaataagatagaggtttatgctc 2085
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2045 ATTAATTAATAATAAAATTAATAAAATGAATTCACATACATTATTGCAATTATATC 2104
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2086 tatt 2089
    |||||
```

Db 2105 TATT 2108

```
RESULT 10
US-08-487-826B-13/C
; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chludis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellem, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelson, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-487-826B-13
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Query Match 1.9%; Score 50; DB 2; Length 19124;
Best Local Similarity 51.3%; Pred. No. 0.015;
Matches 116; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 1871 ttgtttgtgtgtagagttataaataatcataatcattatcgggtgtgttactat 1930
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 15717 TCTTTTGTGTTTATGATATATATATTTTATTTTAAAGTATTTTTCCTC 15658
QY 1931 gccagttcccttataatttaattcctgtttatataatttgaatgtcttatagatttc 1990
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 15657 TTTTGTTTATTTTTTTTAAATCATTTTTTTTTTATATATAAAATTTTTTATTTTT 15598
QY 1991 tttaattctttatagaaacattaaatagaataatcatcatcttaaaatatactacag 2050
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 15597 TTTTGATATATCTTTTTCATTTTATTTATCTATCAAAATTTATATTTTATTAATTTTAT 15538
QY 2051 caaaagcatccaataaglataggttatagttcttatttcttct 2096
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 15537 TATTTTAAATAAATTTTCTCCTTTTATTTTATTTTATTTTATTTTAT 15492
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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: RESULT 11
: US-08-485-284A-1
: Sequence 1, Application US/08485284A
: Patent No. 5750372
: GENERAL INFORMATION:
: APPLICANT: SAKAI, YASUYOSHI
: APPLICANT: TANI, YOSHIMI
: APPLICANT: SHIBANO, YUJI
: APPLICANT: KONDO, HIROTO
: APPLICANT: HATANAKA, HARUYO
: TITLE OF INVENTION: NOVEL VECTOR HAVING PROMOTER THAT IS
: TITLE OF INVENTION: INDUCIBLE BY METHANOL AND/OR GLYCEROL
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
: STREET: 1100 New York Avenue, N.W.
: CITY: Washington
: STATE: D. C.
: COUNTRY: U.S.A.
: ZIP: 20005-3918
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25.
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485,284A
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 43361/1992
: FILING DATE: 28-FEB-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/025,416
: FILING DATE: 01-MAR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: WHITE JR., PAUL E.
: REGISTRATION NUMBER: 32,011
: REFERENCE/DOCKET NUMBER: 217755/FPS38209US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 861-3000
: TELEFAX: (202) 822-0944
: TELEX: 6714627 CUSH
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1667 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: unknown
: MOLECULE TYPE: genomic DNA
: US-08-485-284A-1

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Query Match	1.98	Score 49.8	DB 1	Length 1667
Best Local Similarity	47.88	Pred. No. 0.004		
Matches 144	Conservative	0	Mismatches 157	Indels 0
			Gaps 0	
QY 1861	ttgaacaacatttgcttctgtgtgtagagttataacatcatcatcttatttcgagtgct	1920		
Db 697	TTTAAATAAATAGCGCTGTTCTGTTCTGTTTAAATATATACAAATTTTAACTTAATA	756		
QY 1921	tttagttatgacgcttcctcttatatttaaatcttcgttttatatatatttgaagctct	1980		
Db 757	TTACTCTTTTGGAAATTAATAATTAATTAATATATACATATACCCATATACATTTTAACTATAT	816		
QY 1981	tatagattcttctaattccctctatagacaacatataagaacatcatcatcttaataa	2040		
Db 817	TTTACTATCTAATAAATTAATTCATATTTATTAATTAATTAATTAATTCGCTTAATTAANAATGC	876		
QY 2041	taccttaacagcaagaacatccacaataagatagaggttaatgctccctattttcttcagc	2100		
Db 877	TCCTTTCCATCATCATCATCATCATCATACACAGAGTTTTCGGTTATCAATATACCTTTTAT	936		

QY	2101	tgaataagaatgaacaacagtcgctgggaattctcgaaggggaagcgatggaattatattatc	2160
Db	937	TAACTCTTACGAATTTCAATTATTATTTTATTGACTGCAAAATTTTCATTCATATTTAT	996
QY	2161	t	2161
Db	997	T	997

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RESULT 12
US-08-343-428-1
: Sequence 1, Application US/08343428
: Patent No. 5665586
:
: GENERAL INFORMATION:
: APPLICANT: Nakamura, Etsuo
: APPLICANT: Tsuzuki, Hiroshige
: APPLICANT: Kitadokoro, Kengo
: APPLICANT: Shin, Masaru
: APPLICANT: Teraoka, Hiroshi
: TITLE OF INVENTION: No. 5665586e1 Protease
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: James F. Haley, Jr., Fish & Neave
: STREET: 1251 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10020-1104
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: MS Dos 5.0
: SOFTWARE: Wordperfect 5.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/343,428
: FILING DATE: 18-NOV-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/93/00592
: FILING DATE: 30-APR-1993
: APPLICATION NUMBER: JAPAN 4-126511
: FILING DATE: 19-MAY-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Haley, Jr., James F.
: REGISTRATION NUMBER: 27794
: REFERENCE/DOCKET NUMBER: SHON-7
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212)596-9000
: TELEFAX: (212)596-9090
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2064
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: Genomic DNA
: ORIGINAL SOURCE:
: ORGANISM: Streptomyces fradiae
:
: FEATURE:
: NAME/KEY: -35 signal
: LOCATION: 359..364
: IDENTIFICATION METHOD: by experiment
: NAME/KEY: -10 signal
: LOCATION: 378..383
: IDENTIFICATION METHOD: by experiment
: NAME/KEY: CDS
: LOCATION: 435..1505
: IDENTIFICATION METHOD: by experiment
: NAME/KEY: sig peptide
: LOCATION: 435..944
: IDENTIFICATION METHOD: by experiment

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```

: LENGTH: 636 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: Linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: Pagi692RP
US-08-998-416-1137

Query Match      1.8%. Score 49.2; DB 4; Length 636;
Best Local Similarity 45.2%; Pred. No. 0.0032;
Matches 261; Conservative 0; Mismatches 313; Indels 4; Gaps 2.

OY 1698 taacaatgctacccaactttggcgctaaattatgtaacagaaatgctcaatc 1757
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DB 24 TTATTAACATTAATTAATTAACCTTTTATTATTAATTTTAAGATTAATTAATTAACCTA 83

OY 1758 atagtttaatgctgttttgaanaagccacacatactatccttcttctaataatcc 1817
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 84 TTATATCATTTATTTAATAAATTAATTAATTTGATTTAATAAATCTTAATTAATTAATTAATTA 143

OY 1818 tgcacaatctgcgcctgatcccgaaatcctgnaaatgctcgcctggaacaaattgctt 1877
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 144 TATATTTACTTAATTCATCATTAATTAATTAATTTATTAATTAATTAATAAATAATTAATTAATA 203

OY 1878 tgtgtgttagagttataaatcatltaacttattcgggtgtgtttagctttagccagtt 1937
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 204 TGAATACGATTTAGTCATATGTTCAAAATTTTAAATTAATTAATTAATAAATTAATTAATTAAT 263

OY 1938 ccttaataatccttctgtttatataatcttgaatgctcttataagattccttaaat 1997
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 264 ATTATTTTCTTAAATAAATTAATTAATAATGAAATATCAATAAATTAATAAATTAATTAATTAAT 323

OY 1998 ttccctatagagacccaatataagaa--aactcatcattaaataataccttaacagcaaa 2055
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DB 324 TGTTATTAATAAATATATATTTTATTATTAATTAAGAATTTAATTTTAATTAATTTGTTAA 383

OY 2056 gcatcacaataagatagagggttatabgctccttatttcttcaagctgaatacgaatga 2115
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DB 384 TTATATATTTTATTAATTAATATCATTAATTTTAAATAAATTAATGTTGATTAATTAATTAAT 443

OY 2116 acagtggtggaattctcgaagggaagtgatgaatatatattcttggtggcctttt 2175
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DB 444 CTTTTTAATAAGATTAATTAATTAATAATTTTAACCTTTAATTTCTTAATTAATTAATTTT 503

OY 2176 ccaat--ttacacactgtaaccaattctggtctcggaggtatacactaattctcagta 2233
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DB 504 ATATTATTTAATAATTAATTAATTAATTCATTTTATTAATTAATTAATTAATTAATTAATTAAT 563

OY 2234 ttactgttaattacccaacacagaagccaattattgaa 2271
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DB 564 TAAATTAATATTTTATCATTAATTTAATTAATTAATTAATAA 601

RESULT 14
US-07-945-283-1
Sequence 1, Application US/07945283
Patent No. 5352596
GENERAL INFORMATION:
APPLICANT: Cheung, Andrew K.
APPLICANT: Wesley, Ronald D.
TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants
TITLE OF INVENTION: Involving the EP0 and LRT Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtiss P. Ribando
STREET: 1815 No. 5352596th University Street
CITY: Peoria
STATE: IL
COUNTRY: USA
ZIP: 61604
COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/945,283
; FILING DATE: 19920911
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ribando, Curtis P
; REGISTRATION NUMBER: 27976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 309-685-4011 ext.513
; TELEFAX: 309-685-4128
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8438 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Pseudorabies virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 622..6495
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(1099, "g")
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(1267, "t")
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(1381, "c")
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(1566, "c")
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(7010, "g")
; ORGANISM:
; US-07-945-283-1

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Query Match 1.8%; Score 48; DB 1; Length 8438;  
Best Local Similarity 51.9%; Pred. No. 0.03;  
Matches 108; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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QY 112 gccagccgcctcgtcctcttgagaccatgttgcctgctgctgcggagcttcgcgcctgcga 171
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DB 4493 gccacggctccggcgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacg 4552
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 172 ccgcgcctcgcagagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 231
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4553 gccccggggatgctcctgcggagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 4612
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 232 accgcgaatgggagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 291
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4613 gccccgagagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 4672
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 292 gcattccctcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 319
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4673 ccctcagagacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 4700
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 15  
US-08-998-416-186  
; Sequence 186, Application US/08998416  
; Patent No. 6239264  
; GENERAL INFORMATION:  
; APPLICANT: Philippsen, Peter

```

; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtel, Philipp
; APPLICANT: Rebschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSPYII
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8687
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 615 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1074RP
; US-08-998-416-186

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Query Match 1.8%; Score 47; DB 4; Length 615;  
Best Local Similarity 44.9%; Pred. No. 0.012;  
Matches 259; Conservative 0; Mismatches 315; Indels 3; Gaps 2;

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QY 1698 taacaatgctacccaacttctggcgaataatataatgacacagaatgctccaatc 1757
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DB 24 TATATAAGATATATATATATATATATATATATATATATATATATATATATATATATATAT 83
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QY 1758 atagtttaatggtttgaaagggcacaactatctactatctttcttaaatcc 1817
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 84 TTAATATCATTTATATATATATATATATATATATATATATATATATATATATATATATAT 143
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1818 tgcgaatctctgcccgaatcgcgaatctgaaatctactgcttgacaacaattgctt 1877
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 144 TATATATTTACTTATATATATATATATATATATATATATATATATATATATATATATAT 203
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1878 tctgtctgagttacaatcaatcaatcttacttctcgggtggtttcagttatgcagct 1937
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 204 TGAATATCTATTAGTCTAGTTCGAATTTTAAATTTAGTTTAAATATATATATATATAT 263
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1938 ccttatatttaattctctgtttatataatttgaaatgcttataagattcttaaat 1997
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 264 ATATATTTCTTTATATATATATATATATATATATATATATATATATATATATATATATAT 323
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1998 ttccctagaacataatagaa--aatcattacatttaaatatacattacagcaaaa 2055
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```





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 18, 2002, 02:58:43 ; Search time 2033.22 Seconds  
(without alignments)  
17743.953 Million cell updates/sec

Title: US-09-777-921A-1  
Perfect score: 2673  
Sequence: 1 ccgcacaccgcagcgccgc.....ataccatcatgatctctg 2673

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_estchum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	810.4	30.3	1020	10	BM450214 AGENCOURT
2	765.4	28.6	878	10	BM450214 AGENCOURT
3	732.8	27.4	1117	10	BM460880 AGENCOURT
4	672	25.1	1674	11	AK015371 Mus muscu
5	602	22.5	980	10	BE731210 BE731210
6	558.6	20.9	839	10	BE209622 BE209622
7	527.4	19.7	776	10	BE158686 BE158686
8	522.8	19.6	556	9	BE162667 BE162667
9	503.4	18.8	505	9	AL599428 AL599428
10	493.8	18.5	844	10	BF132795 BF132795
11	484.8	18.1	921	10	BE885075 BE885075
12	471.4	17.6	632	9	BM623288 BM623288
13	462.2	17.3	531	10	BM6894729 BM6894729
14	460.8	17.2	529	10	BM6894680 BM6894680
15	456.4	17.1	740	10	BF168710 BF168710
16	445.4	16.7	839	10	BF570740 BF570740
17	440.6	16.5	930	10	BF582661 BF582661

18	439.4	16.4	506	9	AA001086
19	430.4	16.1	858	10	BF697486
20	424.4	15.9	898	10	BF572032
21	423.4	15.8	720	10	BF773095
22	390.2	14.6	685	10	BF779437
23	389.4	14.6	720	10	BF779437
24	388.8	14.5	682	10	BM491099
25	380.2	14.2	366	10	W39750
26	371.2	13.9	784	10	BE569071
27	369.8	13.8	480	9	AA024208
28	369.2	13.8	853	10	BF538950
29	365.2	13.7	735	10	BF778203
30	365	13.7	501	9	BB853428
31	351.2	13.1	1052	10	AL555731
32	347.2	13.0	518	10	BF473564
33	340	12.7	365	10	W52586
34	340	12.7	519	9	BB855418
35	337	12.6	944	10	BF828204
36	332.8	12.5	437	9	BE127029
37	328.8	12.3	477	9	BB857423
38	326.2	12.2	477	9	BB858108
39	321.2	12.0	750	10	BF623074
40	305.2	11.4	889	10	BF691873
41	303.4	11.4	543	10	BF360178
42	300.6	11.2	940	9	AL555116
43	299	11.2	560	10	BF040514
44	298.8	11.2	859	9	AL564670
45	294.6	11.0	824	10	BF209392

#### ALIGNMENTS

RESULT 1  
BM450214  
LOCUS  
DEFINITION  
AGENCOURT\_6393362 NIH\_MGC\_72 Homo sapiens cdna IMAGE:5528289  
5', mRNA sequence.  
BM450214  
BM450214.1 GI:18499254

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1020)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: ATCC/DCID/DRP  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM12204 row: 0 column: 10  
High quality sequence stop: 619.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="NIH\_MGC\_72"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pCMV-Sport6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2 kb. library constructed by Life  
Technologies."

#### FEATURES

source  
BASE COUNT  
315 a 182 c 269 g 253 t 1 others



Db 421 GCCTTGGTAGAACCTGCATGCAAGGCTCAAGCCATGTTAGAGGTTCCCAACAGCTGAAT 480  
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Db 481 ATGTTGGCCTCTTTCACCAATATTATTTCCAAAGAAAGGAATACCAAGACTTTACAGAGC 540  
QY 1476 ataccaccaactcatgaagtgctccctcgttgtagcatcagltatgtgtttaa 1535  
Db 541 ATCACCCCAACTTCATGAGAGTGCTCCCTGCTAGCAATCACTATGAGTGTATGAA 600  
QY 1536 -aataagaacaaacttaagagagtaaccagaatgatgttgcaatttttgccttaagcct 1554  
Db 601 CAATATGAACCAACTTATAGAGTAACCCAGAAATGATGTGCAATTTTGTCTTACCT 660  
QY 1595 gataatgaacttcaacaatcctcgtgagtgacttttccctcgaatgaacaagtc 1654  
Db 661 GATATTTGAACCTTTCACCAATCTCTGAGTGACTTTTCTCTCGAATGAAACAAAGTC 720  
QY 1655 tatgac-aaagaagctgcatctttt-cacaaagggaagacgtaacaatggtcact 1712  
Db 721 TATGGCAAAAGAAAGCTGCAATTTTTCACAAAGGAGAGATGTAACAATGCTCACTT 780  
QY 1713 caaacctttt-ggactaattatatagtacacagaagatgtcaaaatcagtttaagtgtg 1771  
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QY 1772 ttctgaagaagccacaactatctatctatcctt 1804  
Db 837 TTGAAAAGGCCCAATATTTACTTATCTTCTT 865

RESULT 3  
BM460880 1117 bp mRNA linear EST 05-FEB-2002  
LOCUS AGENCOURT\_6419526 NCL\_CGAP\_Ov44 Mus musculus cDNA clone  
DEFINITION IMAGE:5504225 5', mRNA sequence.  
ACCESSION BM460880  
VERSION BM460880.1 GI:18509920  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgabs-r@mail.nih.gov  
Tissue Procurement: Aaron Hsueh  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1AM12145 row: d column: 18  
High quality sequence stop: 714.  
Location/Qualifiers  
1..1117  
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/db\_xref="taxon:10090"  
/clone="IMAGE:5504225"  
/clone.lib="NCI CGAP Ov44"  
/lab\_host="DH10B (71 phage-resistant)"  
/note="Organ: ovary, FMSG-treated; Vector:  
pCMV-SPORT6.cdb; Site.1: EcoRV; Site.2: NotI. Cloned  
unidirectionally. Primer: Oligo dT. Average insert size  
2.2 kb. Library constructed by Life Technologies. Note:  
this is a NCI CGAP Library."

BASE COUNT 301 a 254 c 297 g 261 t 4 others  
ORIGIN

Query Match 27.4%; Score 732.8; DB 10; Length 1117;  
Best Local Similarity 82.9%; Pred. No. 2,56-113;  
Matches 872; Conservative 0; Mismatches 111; Indels 9; Gaps 3;  
QY 128 ctctggagcaactgttgcgtcgtcggaacttcgcgtcccaaccgctgcagga 187  
Db 46 CCCCCGACCATGCTGGCTGGCTGGCGGGCTTGTGCTGCCACCGCGCTGCCACA 105  
QY 188 cggagagcagcgagcggtcagagacctttccagcatgtgacccgaatggagagc 247  
Db 106 CCGGAGCGCCGACACGCTACGAAAGCCTTCCGGGCGCTGGAACCGCAATGGGGAGG 165  
QY 248 agtgttgacatcggcagcgagcgagcgaagacatgaagacatggcctccctggagca 307  
Db 166 CGTGTGGACATCGGAGAGCTGCAGCAGGGCTCGAAAGCCTGGGCACTCCGCTGGCCA 225  
QY 308 ggaacgagagagaatlttactactgagatgacacaaagatggaaagctggaatc 367  
Db 226 GGACGCGGAGGAGAAATTTTCCACACTGGCGATGTCAAAAGATGGGAAGCTGATTT 285  
QY 368 tgaagaattatgaagtaaccttaagaacatgagaagaatgaatgtgcatttaagag 427  
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QY 608 agacattgaagaatltatccgttctcgtgaacatctcaagaattgacatagggatag 667  
Db 526 AGACATTGAGGAATTTATTCGTTCTTGAAACACTCTACTGGAATGACATAGGGAGAG 585  
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QY 907 acgtcatcaaatgtcctcgtgagacagctgttaattccttgggcatatgaaagtaaca 966  
Db 820 ATGTCAATCAAAATTAATGCTCCGAGACACTGTGAAGTTCTGGGCTTATGACAGACNAG 879  
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Db	1038	CGAAGCGCTTTGGGCTTTTAAAAAGCTACTTT	1089
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AKO15371			
LOCUS			
DEFINITION	AKO15371	1674 bp	mRNA linear HTC 19-JAN-2002
ACCESSION	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930443g12.homolog to PEROXISOMAL CA-DEPENDENT SOLUTE CARRIER, full insert sequence.		
KEYWORDS	AKO15371		
SOURCE	AKO15371.1 GI:12853684		
	HTC; CAP trapper		
	Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone:libB-RIKEN full-length enriched mouse cDNA library		
	clone:4930443g12.		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2 (sites)		
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3 (sites)		
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Kono,H., Akiyama,J., Nishi,K., Kitsuma,T., Tashiro,H., Itoh,M., Sumi.N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kasaiwagi,K., Fujiwaka,E., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawal,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kiru,A. and Hayashizaki,Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4 (sites)		
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 685-690 (2001)		
REFERENCE	5 (bases 1 to 1674)		
AUTHORS	Adachi,T., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Butz,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hangacki,T., Hara,A., Hayatsu,N., Hall,D., Hiramoto,K., Hirooka,T., Horii,F., Hume,D., Imocanti,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Katoh,H., Kawai,T., Kojima,Y., Kono,H., Kouda,M., Koya,S., Kuilhara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ono,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Sakto,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Soabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,Y., Tejima,Y., Toya,T., Yamamura,T., Yananaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama kanagawa 230-0045, Japan (E-mail:genome-res@gs.c.riken.go.jp,		

URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was plimed with a primer [5'-GAGAGGAAGAATCCAGACGCCTCTTTTCTTTTTTAAATAAATTCCTCCCCTC 3']. cDNA was prepared by using triethanolamine thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGGAGATTCTCGCATTAATTAATTAATTCCTCCCCTC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda E1C I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

FEATURES  
Source Location/Qualifiers

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    /db\_xref="taxon:10090"  
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    /sex="male"  
    /tissue\_type="testis"  
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polyA\_site  
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BASE COUNT     479   317   c       428   g       450   t  
ORIGIN

Query Match     25.1%; Score 672; DB 11; Length 1674;  
Best Local Similarity     66.6%; Pred. No. 4,1e-103;  
Matches     979; Conservative     0; Mismatches 485; Indels     6; Gaps     1;

109 ttcggccagcgccctgcgcgcctcgtgcacatcttgctgcgtgcgcgaacttcgcgcctgc 168  
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169 ccacgcgcgcctgcacagagcgcgagacgcgcgcgcgcgtacagagaccctctccagcac 228  
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229 ttgaccgcgaatgggagcggagtgtgtgcacatcgcgcgcgcgtcagagaggcctcaggaacc 288  
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289 ttggatccctcttcggccagagcgccgcggaggaaaattttaactactcttgagatgcaaca 348  
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 DB 349 TGAATTTGCGCTTCAGAGACTGTGCAAAAATGATGATGCGCCATGATGCTTCAGAAA 408  
 QY 469 tgtccaagctctccagaacactggtgtcgtacttcttgaacaaagcagagatgattcc 528  
 DB 409 TAGTCCCTCCCGTGCAGATATTGGGAATCCACATTTCTCTCTCAGGCCCAAGACATCT 468  
 QY 529 ttcaagaactgattggttgaatggagaatgacagtgagctggaaatgagagactact 588  
 DB 469 TGAAGGACATGATTTTGAAGGAGGTGCATGACAGTACAGTGGATGATGAGAGATTTCT 528  
 QY 589 tcttattaatccctgttacaagacattgagaatlaaccgttcttgaacatctcacag 648  
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QY 1429 ttccagcaattattccaaagaagataccaggaacttccagaggcatcaccacaaact 1488  
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RESULT 5  
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 ACCESSION BE731210  
 VERSION BE731210.1 GI:10145202  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 980)  
 NIH-MGC http://imgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Sequencing by: Incycle Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at: image.linl.gov  
 Plate: LLCM534 row: j column: 24  
 High quality sequence stop: 676.  
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 Directionally cloned into EcoRI/XhoI sites using the  
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 for average insert size 1.8kb. Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."  
 BASE COUNT 262 a 232 c 275 g 211 t  
 ORIGIN

Query Match 22.5%; Score 602; DB 10; Length 980;  
 Best Local Similarity 94.1%; Pred. No. 2.3e-91;  
 Matches 726; Conservative 0; Mismatches 30; Indels 16; Gaps 10;

QY 98 cgtgacttctctggcgaagcgccgtcgtcttggacacatttgcgtgctgagga 157  
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Oy 278 gctcaggaacctgggcatccctcttgagccaggaagccggaggaataatttactactg 337  
Db 182 GCTCAGGAACCTGGGCACTCCCTCTGGGCCAGGACGCCGAGGAGAAATTTTACTACTGG 241  
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Oy 458 ggtccagaagaattgcacgtctctccagacactggctgactatttcgaacaagaac 517  
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Oy 577 ggaagagactactcttatttaattcctgttacaagacattgagaagaataatccgtttctga 636  
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Db 774 AT 775

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ACCESSION BF209622  
VERSION BF209622.1 GI:11103208  
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SOURCE human.  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 839)  
NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-rt@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L10M966 row: 9 column: 10

FEATURES  
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Site.1: SfiI (ggccgctggcc); Site.2: SfiI (ggccatattgccc  
); Double-stranded cDNA was prepared from cell line RNA.  
5' and 3' adaptors were used in cloning as follows: 5'  
adaptor sequence: 5'-ATCTAGAGCGCGCGCGCGCATG-dr(30)BN-3'  
(where B = A, C, or G and N = A, C, G, or T). Average  
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies  
contained inserts by PCR. This library was enriched for  
full-length clones and was constructed by Clontech  
Laboratories (Palo Alto, CA)."  
BASE COUNT 243 a 150 c 306 t  
ORIGIN  
Query Match 20.9%; Score 558.6; DB 10; Length 839;  
Best Local Similarity 92.8%; Pred. No. 4.4e-84;  
Matches 675; Conservative 0; Mismatch 39; Indels 13; Gaps 8;  
Oy 1784 cacacaatatcttattcttcttaataatccgcgaatctcgcctgaatccgaa 1843  
Db 1 CACACATTAATCTTATCTTATTAATTCGCAATCTGCTGCTGAAATCGGAA 60  
Oy 1844 tctgaaatgctactgctgtaacaaatctgtgtgtgttagagttlaaatcatlaa 1903  
Db 61 TCTGAAATGTACTGGCTTGAAACAAATTTG-TTGTGTGTATGATTAATCATTTAA 119  
Oy 1904 tcttaattccgggtggttaagttacgttaacgcagttcccttaatatlaattctgttta 1963  
Db 120 TCTTTATTTGCGGTGGTGTATACGTTTATGCACTCTTATTAATTAATTTCTTG-TTTA 178  
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Db 239 TCATTACATTTAAATATATACCTTACAGCAAAAGCATCCAAATATAGATGATATGTC 298  
Oy 2084 cttaattctcttcagctgtaatacgaatgaaacagtggtggaattctgaaagggaagt 2143  
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Oy 2144 atgaatatattattttagagtggaactttccatttaacacatgatacatattggt 2203  
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Db 419 TCCGTGAGTTATACACTATTTTCAGTATATTAGCTTAATTTACACACAAAGCAAT 478  
Oy 2264 ta-cttgaagaatccggttactcctgcaatgcttgaagaacgaggaagaactt 2322  
Db 479 TATTTGAAAGATTCCTGTTATCTGCGCA-TGCTTTGAAAGACAGAGGAAAGCAATTC 537  
Oy 2323 ttgactgtatcagc-ttctcagagacgtttgttcctgttccgttttccctac 2381  
Db 538 TTTCAGCTGATTCAGCTTCTCGAGAGCAATCTTGTTCTCTT-GTCTTGTTCCTAC 595  
Oy 2382 ctttgaacacagatccgtttt---agtcaaggaactcttgggacatctttagtaac 2438  
Db 596 CTTTGAATCAATTCCTTTTATAGTCAAGGAAGACCTCTTGGAACATCTTATGATAC 655  
Oy 2439 ctgaattctcttttaattgataagtgatgatcatgagcaagtgaatggcttat 2498

QY	751	gtctgtctctcgacaacgaacactgcgcccttggagccgtctgaaatcatgaaatcatgaaatc	810
Db	242	GGCGCGCTCTCTGAGACGAGCACCGCTCCCTTGGATCGCCTCAAGCTCATGATGACAGCTTC	301
QY	811	acggttcaaatcagacaacaaatgaacatatttgggtgttgcgaagtgtgtaaaagag	870
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QY	871	ga-9gtaccgcgtcgcttggaggggaaatggtacaaacgtcatcaaatatgcttcctag	929
Db	356	GACGGAATCCGTTCCCTTTGGAGAGAATGGCACCATGTTCATCAATAATAGCTCCGAG	415
QY	930	acagctgttaaatcttgggcacatgacaagtaacaagaagtactactgaagaagagaca	989
Db	416	ACAGCTGTGAAGTTCTGGGCTTATGAMACAGTACAGAAGAGTTGCTTACCGAGAGAAGACAA	475
QY	990	a-aatagaagaacttggagagatattttcttgggttccatgctgtgtagaagaactgcacag	1048
Db	476	ACAATTAGGAGACCTTGGAGAGGTTTATCTCTGGTTCATGGCTGGAGCAACTGCTCAGAC	535
QY	1049	ttttatataccaatgagaggtatgaaacaacagcgtgctgtgagcaaacactggcagta	1108
Db	556	TTTTTATTACCCCATGAGAGGTTTTCAAAACCCGCTACTGTAGCCAAAACCTGACATTA	595
QY	1109	ctctggaatatagtattgtgccaaagaagatttgaacatgaaggcttggagctttta	1168
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QY	1169	caagagctatgttcccaattta-ttagtatcatatccctatgcaagcgtatgacttgcgtg	1227
Db	655	CAAAAGCTTACATTCCTCAATTTTACGAGGCATCATTCCTTACGCAAGCATGATCTCGCTG	714
QY	1228	tgtacgagctcttgaagtcctattggcgcgga-taatttgcaaaagattcgttaaaccc	1285
Db	715	TGTACGACCTTTTGAGTCTTATCGGCTTGAGATTAACTTTGCCAANAAGACTCGGTCAACC	773
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BI962667			
LOCUS			
DEFINITION	BI962667	556 bp	mrna
	1e53b05.y1	Melton Normalized Human Islet 4 N4-HIS 1	linear
	cDNA 5'	similar to TR:09066 Q9066	HYPOTHEITICAL 11.3 KD PROTEIN.
			;', mRNA sequence.
ACCESSION	BI962667		
VERSION	BI962667.1	GI:16337072	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	human sapiens		
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;		
	Mammalia: Eutheria: Primates: Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 556)		
	Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,		
	Lemishka, I., Seearce, M., Bresciani, J., Gradwohl, G., Clifton, S.,		
	Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blstein, A.,		
	Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J., Cardenas		
	, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,		
	Jackson, Y. and Bowers, Y.		
	Endocrine Pancreas Consortium		
TITLE	Unpublished (2000)		
JOURNAL	Other-ESTs: 1e53b05.x1		
COMMENT	Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue		
	Endocrine Pancreas Consortium		
	Harvard University, Howard Hughes Medical Institute		
	Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,		
	MA 02138		
	Tel: 617-495-1812		
	Fax: 617-495-8557		
	Email: dmelton@iobhp.harvard.edu		
	Library was constructed by Dr. Douglas Melton DNA sequencing by:		
	Washington University Genome Sequencing Center For information on		
	obtaining a clone please contact: Juliana Brown		
	(brown@fas.harvard.edu)		







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QY 601 cgttcaagacattggaataattccgttcttcgtgaacaattctacagaattgacatag 660
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Db 361 CTGTTACAGACATTTGAGGAATTTATCCGTTTCTGGAAACATTTCTACAGGAATTGACATAG 420
QY 661 gggatgcttaactatctccagatgatctcagcggaagaagcaaaaaaacccgagacaatgct 720
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Db 421 GGGATGCTTAATTAATTTCCAGATGAATTCACGGAGACGAAAAAATCCGGCAATATGT 480
QY 721 ggaagcagcttttgcgagagagcat 745
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Db 481 GGAGCAGCTTTTGGCAGAGGCAAT 505

RESULT 10
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LOCUS 601645924F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102109 5',
DEFINITION mRNA sequence.
ACCESSION BF132795
VERSION BF132795.1 GI:10971835
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 844)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L16M974 row: o column: 06
High quality sequence stop: 534.
Location/Qualifiers
1..844
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4102109"
/clone_lib="NIH_MGC_59"
/tissue_type="nucoepidermoid carcinoma"
/lab_host="DH10B (PI phage-resistant)"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgcgcgcgcgc); Site_2: SfiI (ggcgcattagcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGCACATG-dT(30)BN-3'
(where B = A, C, G, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
library."
BASE COUNT 233 a 148 c 168 g 295 t
ORIGIN
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QY 1644 tgaacaagctctatgcaaaagaagctgtcttttccaaaaaggaagcgttaaca 1703
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Db 61 TGAACAAGCTATGCGAAAGAGCTGACATTTTTCACAAAAGGGAAGTGTACAA 120
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QY 1704 tggctacttcaaaacttttgggtctaattatataatgtaacacgaagaagtgccaatcatagtc 1763
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Db 121 TGGCACTTCAAAAC-TTTGGCTTAATTAATTAATGACACAGAAAGTTCAAAATCATAGTT 179
QY 1764 ttaatgtctttgaaaaggccacacaacttaacttctcttcttctaatactcgtcaaa 1823
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Db 180 TTAATGTG-TTTGAAGAAAGCCACACAAATTAATCTTATCTTTTCTTAATTAATCTGCAAA 238
QY 1824 tcttcgcccgtgaatcgaatctgaaaaatgtaactgcttgtaacaaaaatttgcttgctg 1883
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Db 239 TCTCTGCCCTGAATCCGAAATCTGAATAATGACTGCGTTGAACAAATTTGTTGTGAG-- 296
QY 1884 ttgagatgaataatcatatcatcttattcttggtggtgttgtaagttatgccaagtcctta 1943
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Db 297 -TAGAGTTAATAAACAATTAATCTTAATTTGGGGGTGAGTTAGCTTAAGCCAGTTCTTTA 355
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Db 533 GGAAATTTCTG-AGGGAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 590
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RESULT 11
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LOCUS 601510825F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912103 5',
DEFINITION mRNA sequence.
ACCESSION BE885075
VERSION BE885075.1 GI:10333851
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 921)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L16M9730 row: b column: 08
High quality sequence stop: 534.
Location/Qualifiers
1..921
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3912103"
/clone_lib="NIH_MGC_71"
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FEATURES

source



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Db	45	ccccggagaccatgcctgcctgcctcgccgaccttttgtcctcccacccgcgcctgcacaca	104
OY	188	cgcggagacagccgcgccttacgagaccctctccaggcatcgcgcgcgaacgcgaatgggagcg	247
Db	105	cgcggagacccgcgcacgcctnagaaacgctctccgggcgccttgagacgcgaatgggagaccg	164
OY	248	agtgttgacatcggcgcgcctgcagaggggctcagaacccctgggcatccctctggacca	307
Db	165	cgtgttgacatcgcgcgcctgcagagggctcagacagggcctgcgaaacccctgggcatccctctggacca	224
OY	308	ggagccgcgagagaaaatttttctaactacgtagaatgtlcaacaagaatgggaacgtgatatt	367
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OY	368	tgaagaatttatgaagtacctaagaacatagaagaagaatagaattggcatlaagaag	427
Db	285	tgaagaattttatgaatatnacttaaaagaccatagagaagaaaaatgaatttngcattttaanaag	344
OY	428	tttagacaaaataatgatgtgnaaaaatttgaggtctcagaattgtccagctctccagac	487
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OY	488	actggtctgcatattctctgnaacaaacagcagagttgatcttccaagcatgtatgtga	547
Db	405	gctcgttttacctatattttttgaaaamcacagacgtctgatttttcaaagcatnagaccttga	464
OY	548	tggagcaatgcagctgagctgnaatgaatgtgagagacactctatataacccgtctac	607
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OY	608	agacattgaggaataatcgcgttctcggnaacatctcaggaattgacatagggagatag	667
Db	525	agacattgaggaataatnattccgtttctggaacacactctnctgsaatttgacatagggatag	584
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DEFINITION	35456 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.		
ACCESSION	BG894729		
VERSION	BG894729.1 GI:14304970		
KEYWORDS	EST.		
SOURCE	pig.		
ORGANISM	Sus scrofa		
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	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
REFERENCE	1 (bases 1 to 531)		
AUTHORS	Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.		
TITLE	Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine		
JOURNAL COMMENT	Unpublished (2000) Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@emil.marc.usda.gov Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross-match with the -minscore 18 and -mismatch 12 options. PCR primers FORWARD: AGGAACAAGCATATGACCAT BACKWARD: GTTTTCCCACTGCAGCG Plate: 119 row: K column: 13 Seq primer: ATTTAGGTGACACTATAG.		

FEATURES		Location/Qualifiers
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ORIGIN		
Query Match	17.3%; Score 462.2; DB 10; Length 531;	
Best Local Similarity	91.9%; Pred. No. 6.8e-68;	
Matches 488:	Conservative 0; Mismatches 43; Indels 0; Gaps 0;	
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DB	1 AAGCATGTGTCGTGATGGACAAATGACAGTGCATCGAATGATGAGGAGCATTCTTTCT	60
OY	593 attaatccgtgtcaagaacattgaggaaattccgtttctgaaaaccttcaaggat	652
DB	61 ATTATATCCCGTTACAGACATTGAGGAATTTATCCGTTCTTGAAACATTCTTACCGGTAT	120
OY	653 tgacataaggagatagctttaactaccagatgaattcacagagacgaaaaaaatccgg	712
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OY	833 gaacatatctgtgtgctttcgacagatggtlaaagaagaggtalcgcgtcgctttgag	892
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DB	361 AGGAATATGTTACMAATGTCATTAATTAATTCGCCCTGAGACAGCTGTTAAGTTCTGGGCATA	420
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VERSION	BG894680.1 GI:14304921	
KEYWORDS	EST.	
SOURCE	pig.	
ORGANISM	Sus scrofa	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.	
REFERENCE	1 (bases 1 to 529)	
AUTHORS	Fahrenkrug,S.C., Fekling,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keeler,J.W.	
TITLE	Design and use of two pooled tissue normalized cdna libraries for EST discovery in swine	
JOURNAL	Unpublished (2000)	



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Db 416 TGACTGGAAATGAATGAGGAGATTACTTTTATTTAACCTGTGACAGACTTGAGGAAA 475
QY 622 ttatcgtttctcggaaacattctacaggaattgacatagggatagcttaactatccag 681
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QY 682 atgaattcaaggaagacgaaaaaatc-cggacatgggtggagcaagctttggcagga 740
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Search completed: August 18, 2002, 07:16:47  
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